

GenCore version 5.1.3
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OM protein - protein search, using sw model
 Run on: January 2, 2003, 12:04:54 ; search time 11 seconds
 (without alignments)
 27.566 Million cell updates/sec

Title: US-09-824-053-3
Perfect score: 77
Sequence: 1 DLPMSPRGVIASNLXFF 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117078 seqs, 18951520 residues
Total number of hits satisfying chosen parameters: 117078
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database : Published Applications_AA:*

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3: /cgn2_6/ptodata/2/pupaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pupaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pupaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pupaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pupaa/PC015_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/2/pupaa/US10_NEW_PUB.pep:*
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13: /cgn2_6/ptodata/2/pupaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pupaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	75	97.4	16	10 US-09-824-053-3
2	75	97.4	546	10 US-09-998-284-2
3	75	97.4	546	10 US-09-824-053-31
4	74	96.1	16	10 US-09-824-053-10
5	40	51.9	1884	10 US-09-785-770A-17
6	40	51.9	1907	10 US-09-785-770A-16
7	39	50.6	160	US-09-764-864-1020
8	39	50.6	442	10 US-09-731-872-286
9	39	50.6	468	10 US-09-731-872-283
10	39	50.6	468	10 US-09-933-561-2
11	38	49.4	393	9 US-10-030-185-10
12	38	49.4	609	10 US-09-815-442-10740
13	38	49.4	793	10 US-09-925-302-780
14	38	49.4	4545	10 US-09-873-403-2
15	37	48.1	44	10 US-09-864-761-30590
16	37	48.1	119	10 US-09-867-550-245
17	37	48.1	607	10 US-09-815-242-13379
18	37	48.1	607	10 US-09-815-442-13682
19	37	48.1	637	10 US-09-815-242-12058

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-09-824-053

FILING DATE: 03-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08-669,304

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Stanislaus Aksman

REGISTRATION NUMBER: 28 562

REFERENCE/DOCKET NUMBER: <Unknown>

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 955-926

TELEFAX: (202) 778-2201

TELEX: No. US20020106725A1

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

Sequence 9, Appl1	Sequence 28, Appl
Sequence 10, US-09-801-196-28	Sequence 33, Appl
Sequence 9, US-09-835-996-33	Sequence 4, Appl
Sequence 11, US-10-067-534-3	Sequence 36754, A
Sequence 12, US-10-077-761-36754	Sequence 8, Appl
Sequence 13, US-10-077-814-4	Sequence 6, Appl
Sequence 14, US-09-738-626-5827	Sequence 1030, AP
Sequence 15, US-09-730-626-3550	Sequence 3550, AP
Sequence 16, US-09-817-676A-14	Sequence 2, Appl
Sequence 17, US-09-910-516-4	Sequence 14, Appl
Sequence 18, US-09-995-542-12	Sequence 415, Appl
Sequence 19, US-09-995-542-10	Sequence 39604, A
Sequence 20, US-09-759-5089-2	Sequence 5827, AP
Sequence 21, US-09-764-1030	Sequence 10, AP
Sequence 22, US-10-035-027-4	Sequence 4, Appl
Sequence 23, US-09-864-761-43603	Sequence 43603, A
Sequence 24, US-09-764-877-1246	Sequence 1246, AP
Sequence 25, US-09-798-692-1793	Sequence 1793, AP
Sequence 26, US-09-798-692-2057	Sequence 2057, AP

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 ; MOLECULE TYPE: Peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 ; US-09-824-053-3
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 ; Query Match 97.4%; Score 75; DB 10; Length 16;
 ; Best Local Similarity 100.0%; Pred. No. 5e-07; 0; Mismatches 0; Indels 0; Gaps 0;
 ; Matches 16; Conservative 0;
 ;
 ; OY 1 DLPMSPRGVIASNLXF 16
 ; Db 1 DLPMSPRGVIASNLXF 16
 ;
 ; RESULT 2
 ; US-09-998-284-2
 ; Sequence 2, Application US/09998284
 ; Patent No. US20020106725A1
 ; GENERAL INFORMATION:
 ; APPLICANT: POUlsen, et al.
 ; TITLE OF INVENTION: COMPOSITION
 ; FILE REFERENCE: 67459-2035
 ; CURRENT APPLICATION NUMBER: US/09/998,284
 ; CURRENT FILING DATE: 2001-11-30
 ; PRIOR APPLICATION NUMBER: PCT/IB00/00829
 ; PRIOR FILING DATE: 2000-06-02
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 546
 ; TYPE: PRT
 ; ORGANISM: Chondrus crispus
 ; US-09-998-284-2
 ;
 ; RESULT 3
 ; US-09-824-053-31
 ; Sequence 31, Application US/09824053
 ; Patent No. US20020106725A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Peter Stougaard
 ; TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A
 ; NUMBER OF SEQUENCES: 34
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hunton & Williams
 ; STREET: 1900 K Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20006-1109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/824,053
 ; FILING DATE: 03-Apr-2001
 ; CLASSIFICATION: <Unknown>
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/669,304
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Stanislaus Aksman
 ; REGISTRATION NUMBER: 28,562
 ;
 ; REFERENCE/POCKET NUMBER: <Unknown>
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 955-1926
 ; TELEX: (202) 778-2201
 ; TELEX: NO. US20020106725A1e
 ; INFORMATION FOR SEQ ID NO: 10:
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 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ;
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: Peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 ; US-09-824-053-10

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 Best Local Similarity 93.8%; Pred. No. 7.4e-07; 0; Mismatches
 Matches 15; Conservative 1; Indels 0; Gaps 0;

Qy 1 DLPMSPRGVIAASNLXF 16
 Db 1 DLPMSPRGVIAASNLWF 16

RESULT 5
US-09-785-770A-17
 Sequence 17, Application US/09785770A
 GENERAL INFORMATION:
 Patent No. US20020103360A1
 APPLICANT: Pan, Yang
 APPLICANT: Barnes, Thomas M.
 TITLE OF INVENTION: A NOVEL PROTEIN RELATED TO MELANOMA-INHIBITING PROTEIN
 TITLE OF INVENTION: AND USES THEREOF
 FILE REFERENCE: 07334-288001
 CURRENT APPLICATION NUMBER: US/09-785-770A
 CURRENT FILING DATE: 2001-07-16
 PRIORITY FILING DATE: 1999-09-01
 PRIORITY FILING DATE: 1998-09-01
 PRIORITY APPLICATION NUMBER: US 09/145,056
 NUMBER OF SEQ ID NOS: 24
 SEQ ID NO 17
 LENGTH: 1884
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-785-770A-17

Query Match 51.9%; Score 40; DB 10; Length 1884;
 Best Local Similarity 43.8%; Pred. No. 90; 3; Mismatches 6; Indels 0; Gaps 0;

Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DLPMSPRGVIAASNLXF 16
 Db 1804 DLPLHPRGFLPGHAFP 1819

RESULT 6
US-09-785-770A-16
 Sequence 16, Application US/09785770A
 General Information:
 Patent No. US20020103360A1

GENERAL INFORMATION:
 APPLICANT: Barnes, Thomas M.
 TITLE OF INVENTION: A NOVEL PROTEIN RELATED TO MELANOMA-INHIBITING PROTEIN
 TITLE OF INVENTION: AND USES THEREOF
 FILE REFERENCE: 07334-288001
 CURRENT APPLICATION NUMBER: US/09-785-770A
 CURRENT FILING DATE: 2001-02-16
 PRIORITY FILING DATE: 1999-09-01
 PRIORITY APPLICATION NUMBER: US 09/387,462
 PRIORITY FILING DATE: 1998-09-01
 NUMBER OF SEQ ID NOS: 24
 SEQ ID NO 16
 LENGTH: 1907
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-785-770A-16

Query Match 51.9%; Score 40; DB 10; Length 1907;
 Best Local Similarity 43.8%; Pred. No. 92; 6; Mismatches 6; Indels 0; Gaps 0;

Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DLPMSPRGVIAASNLXF 16
 Db 176 NLPLSPQGTVRATVEF 191

RESULT 9
US-09-731-872-283
 Sequence 283, Application US/09731872

Patent No. US20020102004A1
 GENERAL INFORMATION:
 APPLICANT: Dumas Milne Edwards, Jean Baptiste
 APPLICANT: Bouquelert, Lydie
 APPLICANT: Jobert, Severin
 TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
 FILE REFERENCE: 78 US3. REG
 CURRENT APPLICATION NUMBER: US/09/731,872
 CURRENT FILING DATE: 2000-12-07
 PRIOR APPLICATION NUMBER: US 60/169,629
 PRIOR FILING DATE: 1999-12-08
 PRIOR APPLICATION NUMBER: US 60/187,470
 PRIOR FILING DATE: 2000-03-06
 NUMBER OF SEQ ID NOS: 482
 SOFTWARE: Patent.pm
 SEQ ID NO: 283
 LENGTH: 468
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: NAME/KEY: SIGNAL
 LOCATION: -21..-1
 9-731-872-283

Query Match Score 50 %; DB 10; Length 468;
 Best Local Similarity 37.5%; Pred. No. 29;
 Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DLPMSPRGVIASNLXF 16
 :||:||: : :|
 Db 176 NLPLSPQGTVRTAVF 191

RESULT 10
 US-99-933-561-2
 Sequence 2, Application US/09933561
 ;
 PATENT NO. US20020106664A1
 ;
 GENERAL INFORMATION:
 APPLICANT: Lal, Preeti G.
 APPLICANT: Kaser, Matthew R.
 APPLICANT: Baughn, Mariah R.
 TITLE OF INVENTION: TRAPASIN-LIKE PROTEIN
 FILE REFERENCE: PC-0002-1 CIP
 CURRENT APPLICATION NUMBER: US/09/933,561
 CURRENT FILING DATE: 2001-08-20
 PRIOR APPLICATION NUMBER: 09/292,097
 PRIOR FILING DATE: 1999-04-14
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PERL Program
 LENGTH: 468
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: NAME/KEY: VARIANT
 OTHER INFORMATION: 103348CD1
 09-933-561-2

Query Match Score 50.6%; DB 10; Length 468;
 Best Local Similarity 37.5%; Pred. No. 29;
 Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DLPMSPRGVIASNLXF 16
 :||:||: : :|
 Db 176 NLPLSPQGTVRTAVF 191

RESULT 11
 US-10-090-185-10
 Sequence 10, Application US/10090185
 ;
 Publication No. US20020197647A1
 ;
 GENERAL INFORMATION:
 APPLICANT: Zhang, Xiaokui
 APPLICANT: Wrzeszczynska, Melissa R

Query Match Score 49.4%; DB 9; Length 393;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLPMSPR 7
 |||||
 Db 346 DLPMSPR 352

RESULT 12
 US-09-815-242-10740
 ; Sequence 10740, Application US/09815242
 ;
 PATENT NO. US20020061569A1
 ;
 GENERAL INFORMATION:
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: Identification of Essential Genes in
 FILE REFERENCE: ELUTRA.011A
 CURRENT APPLICATION NUMBER: US/09/815,242
 CURRENT FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 14110
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 10740
 LENGTH: 609
 TYPE: PRT
 ORGANISM: Enterococcus faecalis
 FEATURE: NAME/KEY: VARIANT
 LOCATION: (1)..(609)
 OTHER INFORMATION: Xaa = Any Amino Acid
 US-09-815-242-10740

Query Match Score 49.4%; DB 10; Length 609;
 Best Local Similarity 43.8%; Pred. No. 57;
 Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

RESULT 13
US-09-925-302-780
Sequence 780, Application US/099253302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925-302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 780
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-925-302-780

Query Match 49.4%; Score 38; DB 10; Length 793;
Best Local Similarity 100.0%; Pred. No. 76; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLPMSPR 7
Db 746 DLPMSPR 752

RESULT 14
US-09-973-403-2
; Sequence 2, Application US/09873403
; PATENT NO. US20020058207A1
; GENERAL INFORMATION:
; APPLICANT: SIVASTAVA, Premad K
; TITLE OF INVENTION: COMPLEXES OF ALPHA (2) MACROGLOBULIN AND ANTIGENIC
; MOLECULES FOR IMMUNOTHERAPY
; FILE REFERENCE: 8446-178
; CURRENT APPLICATION NUMBER: US/09/873,403
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 09/625,139
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/209,266
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO: 2
; LENGTH: 4545
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-873-403-2

Query Match 49.4%; Score 38; DB 10; Length 4545;
Best Local Similarity 54.5%; Pred. No. 5.2e+02; Mismatches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DLPMSPRGVIA 11
Db 2460 DLPOQPMGIA 2470

RESULT 15
US-09-864-761-36590
Sequence 36590, Application US/09864761
; Patent No. US20020048763A1

Query Match 48.1%; Score 37; DB 10; Length 44;
Best Local Similarity 58.3%; Pred. No. 4.6; Mismatches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PMSPRGVIASNL 14

GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acornix X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/US01/06667
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/235,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/06668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/06669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/06665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/06663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/06662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/06661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/06670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: annotrax sequence Listing Engine vers. 1.1
; SEQ ID NO: 36590
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: SWISSPROT HIT: P77672, EVALUE 2.10e+00
; OTHER INFORMATION: EST_HUMAN HIT: BE960561.1, EVALUE 1.80e+00
; US-09-864-761-36590

Db 4 ||||: :|: PRIOR APPLICATION NUMBER: 60/269, 308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 13379
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; US-09-815-242-13379

Query Match 48.1%; Score 37; DB 10; Length 607;
Best Local Similarity 37.5%; Pred. No. 84; Mismatches 6; Indels 0; Gaps 0;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DLPMSPRGVIASNLXF 16
Db 431 DIPAAPRGIPQIPEVTF 446

RESULT 17
US-09-815-242-13379
; Sequence 13379, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELTRA.01A
; CURRENT APPLICATION NUMBER: US/09/815, 242
; PRIOR APPLICATION NUMBER: 60/191, 078
; PRIOR FILING DATE: 2000-03-21
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/206, 848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207, 727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242, 578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253, 625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257, 931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269, 308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 13682
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; US-09-815-242-13682

Query Match 48.1%; Score 37; DB 10; Length 607;
Best Local Similarity 37.5%; Pred. No. 84; Mismatches 6; Indels 0; Gaps 0;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DLPMSPRGVIASNLXF 16
Db 431 DITAAPRGIPQIPEVTF 446

RESULT 19
US-09-815-242-12058
; Sequence 12058, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.

TITLE OF INVENTION: Identification of Essential Genes in
 TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A
 CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/227,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12058
 LENGTH: 637
 TYPE: PRT

; ORGANISM: *Pseudomonas aeruginosa*
 ; US-09-815-242-12058

Query Match Score 40.1%; Best Local Similarity 43.8%; Matches 7; Conservative 3; Mismatches 6; Gaps 0;

Qy 1 DLPPSPRGVIAASNXF 16
 Db 461 DIPPAAPRQVQIETWF 476

RESULT 20

S-09-975-139-9
 Sequence 9, Application US/09975139
 Patent No. US2002155460A1

GENERAL INFORMATION:

APPLICANT: Genencor International, Inc.
 APPLICANT: Schellenberger, Volker
 APPLICANT: Naki, Donald
 APPLICANT: Morrison, Thomas B.
 TITLE OF INVENTION: INFORMATION RICH LIBRARIES

FILE REFERENCE: 23623-060

CURRENT APPLICATION NUMBER: US/09/975,139

CURRENT FILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/239,476

PRIOR FILING DATE: 2000-10-10

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 4.0

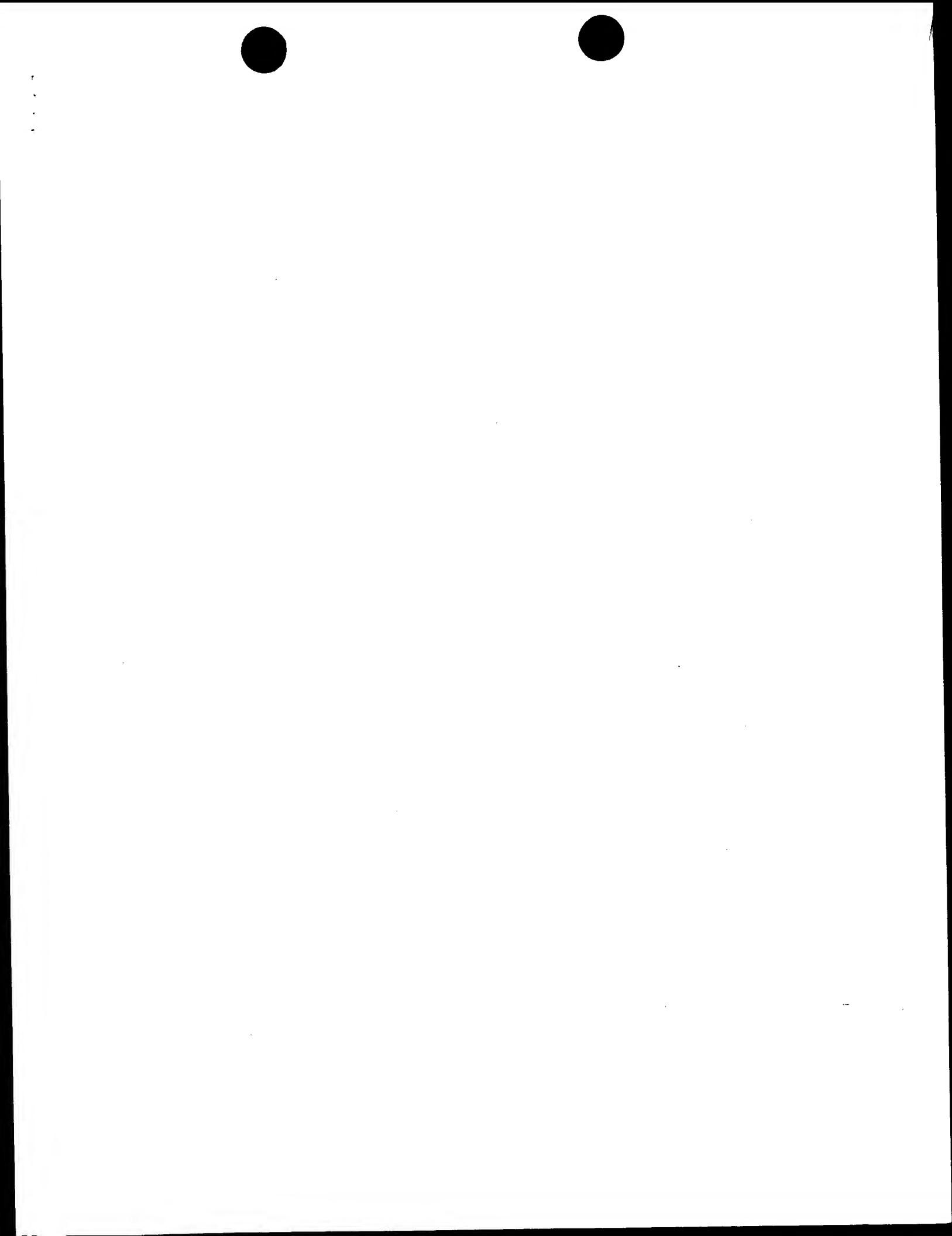
SEQ ID NO 9
 LENGTH: 388
 TYPE: PRT

; ORGANISM: *Yersinia enterolitica*
 ; FEATURE: AMPC protein
 ; OTHER INFORMATION: AmpC protein
 ; US-09-975-139-9

Query Match Score 46.0%; Best Local Similarity 54.5%; Matches 6;保守型 4; 错配型 1; 缺失型 0; 插入型 0;

QY 3 PMSPRGVIAASN 13
 |:::|::|::|:
 Db 304 PINPQGVIAIDS 314

Search completed: January 2, 2003, 12:10:23
 Job time : 12 secs



DR WPI: 1997-052332/05.

XX Recombinant production of polypeptide having hexose oxidase activity
PT - used in food preparations as antibacterial and antioxidant agent

XX PS Claim 6; Page 99; 124pp; English.

AAW20068-75 are small peptides derived from hexose oxidase (HO) of the marine algae species Chondrus crispus. Hexose oxidase and peptides having HO activity are useful in the production of food products, e.g. dairy products, starch-containing food products (dough) and non-dairy beverages. HO and active peptide fragments have antimicrobial and antioxidant properties and act by removing all the oxygen in a food packaging. HO and peptides of HO can also be used in an animal feed, especially silage. Further uses are to reduce, or analyse, the sugar content in a food, in the production of cosmetics, tooth care products or a pharmaceutical product and in lactone production. HO can be recombinantly produced in industrially appropriate quantities, and at a quality and purity level which renders the polypeptide suitable for industrial purposes.

Sequence 16 AA;

Query Match: 97.4%; Score: 75; DB: 18; Length: 16;
Best Local Similarity: 100.0%; Pred. No: 9.9e-07;
Matches: 16; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

OY 1 DLPMSPRGVIAASNLXF 16
Db 1 DLPMSPRGVIAASNLXF 16

RESULT 2

AAW20076 ID AAW20076 standard; Protein: 546 AA.

AC XX AC AAY83619
XX AC AAY83619;

DT 12-SEP-1997 (first entry)

DE Hexose oxidase, an antimicrobial/antioxidant agent.

XX KW Hexose oxidase; Chondrus crispus; marine algae; recombinant; antimicrobial; antioxidant; food preparation; dairy product; starch; beverage; animal feed; silage; sugar reduction; cosmetics; dental; toothpaste; dough; lactone production.

XX OS Chondrus crispus.

PN WO9640935-A1.

XX PN 19-DEC-1996.

XX ID 04-JUN-1996; 96WO-DK00238.

XX ID 07-JUN-1995; 95US-0476910.

XX PA (BIOT-) BIOTEKNOLOGISK INST.

XX PI Hansen OC, Stougaard P;

XX DR WPI: 1997-052332/05.

XX DR N-PSDB; AAT76552.

XX PT Recombinant production of polypeptide having hexose oxidase activity - used in food preparations as antibacterial and antioxidant agent

XX PS Example 3, 5; Page 95-97; 124pp; English.

AAW20076 shows the hexose oxidase (HO) enzyme of the marine algae species Chondrus crispus. HO is useful in the production of food products, e.g. dairy products, starch-containing food products (dough) and non-dairy beverages. HO and active peptide fragments have

CC antimicrobial and antioxidant properties and act by removing all the oxygen in a food packaging. HO and peptides of HO can also be used in an

CC animal feed, especially silage. Further uses are to reduce, or analyse, the sugar content in a food, in the production of cosmetics, tooth care products or a pharmaceutical product and in lactone production. HO can

CC be recombinantly produced in industrially appropriate quantities, and at a quality and purity level which renders the polypeptide suitable for industrial purposes.

CC Query Match: 97.4%; Score: 75; DB: 18; Length: 546;
CC Best Local Similarity: 93.8%; Pred. No: 5.3e-05;
CC Matches: 15; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;

CC OY 1 DLPMSPRGVIAASNLXF 16
Db 219 DLPMSPRGVIAASNLXF 234

RESULT 3

CC AAY83619 ID AAY83619 standard; Protein: 546 AA.

CC XX AC AAY83619;

CC DT 29-AUG-2000 (first entry)

CC DR Synthetic hexose oxidase.

CC KW Hexose oxidase; production; fermentation; synthetic; modification; prokaryote; eukaryote.

CC OS Synthetic.

CC PN EP1008651-A2.

CC PD 14-JUN-2000.

CC PP 01-D8C-1999; 99EP-0204668.

CC PR 09-DEC-1998; 98DK-0001630.

CC PA (BIOT-) BIOTEKNOLOGISK INST.

CC PI Stougaard P, Pedersen LH, Wolff AM, Poulsen U, Hansen OC;

CC DR WPI: 2000-389309/34.

CC DR N-PSDB; AAT76552.

CC PT Nucleic acid fragment useful for producing large amounts of hexose oxidase comprises nucleotide sequence encoding hexose oxidase that is modified by at least one codon

CC PS Disclosure; Page 28-29; 42pp; English.

CC CC Wild type hexose oxidase can be produced by isolating a nucleotide sequence coding for hexose oxidase naturally produced by an organism and modifying the sequence so that the modified sequence is expressed, under identical conditions, at a level at least 10% higher than the non-modified sequence. The method is useful for producing hexose oxidase in prokaryotic and eukaryotic cells. Previous methods of producing hexose oxidase were to isolate the enzyme from a source that naturally produces the enzyme, using host organisms which produce a relatively low level of expression. Therefore, industrial production of the enzyme is not feasible using this method. This is a much improved method which produces at least 250 mg enzyme per liter of fermentation medium.

CC SQ Sequence 546 AA;

CC Query Match: 97.4%; Score: 75; DB: 21; Length: 546;
CC Best Local Similarity: 93.8%; Pred. No: 5.3e-05;

SQ	Sequence	546 AA'
Qy	1 DLIMSPRAVIAASLXF 16	Score 75; DB 22; Length 546; Best Local Similarity 93.8%; Pred. No. 5; Je-05; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db	219 DLPMSPRQVIAASNLHF 234	
		RESULT 5
AA59205	AAB59205 standard; Protein; 546 AA.	
ID	AAB59205 standard; Protein; 546 AA.	
XX		
AC	AAB59205;	
XX		
DT	23-MAR-2001 (first entry)	
XX		
DE	Chondrus crispus hexose oxidase enzyme protein.	
XX		
KW	Hexose oxidase; marine alga; anti-fouling.	
XX		
OS	Chondrus crispus.	
XX		
PN	WO200075293-A2.	
XX		
PD	14-DEC-2000.	
XX		
PF	02-JUN-2000; 2000WO-1B000829.	
XX		
PR	04-JUN-1999; 99GB-0013050.	
XX		
PA	(DANI-) DANISCO AS.	
XX		
PI	Poulsen CH, Kragh KM;	
XX		
DR	WPI; 2001-112148/12.	
XX		
PT	New anti-fouling composition, useful as a coating for treating different surfaces, e.g. outdoor woodwork, external surface of a central heating system, or a hull of a marine vessel -	
PT		
PS	Claim 5: Page 35-36; 36pp; English.	
CC	The present invention relates to a new anti-fouling composition. The composition involves a surface coating material, a hexose oxidase	
CC	enzyme obtained from a marine organism and a substrate for the enzyme. The anti-fouling composition is useful as a coating formulated	
CC	for treating a surface, e.g. outdoor wood work, external surface of a central heating system, or a hull of a marine vessel. It is also useful as an anti-fouling agent for marine structures exposed to seawater flora and fauna.	
CC		
SQ	Sequence 546 AA;	

XX Streptococcus polypeptide SEQ ID NO 10084.
DE XX KW Group B streptococcus; Streptococcus agalactiae; protein antigen;
KW Streptococcus; GAS; GBS; group B streptococcus; streptococcus agalactiae;
KW group A streptococcus; Streptococcus Pyogenes; antibacterial; antiinflammatory;
KW infection; vaccine; meningitis; gene therapy.
XX OS XX KW Vaccine; screening; immunogen; detection; diagnosis; infection;
OS Streptococcus agalactiae.
XX Streptococcus agalactiae.
XX WO200234771-A2.
XX PD 02-MAY-2002.
XX XX PR 29-OCT-2001; 2001WO-GB04789.
XX PP 27-OCT-2000; 2000GB-0026333.
XX PR 24-NOV-2000; 2000GB-0028727.
XX PR 07-MAR-2001; 2001GB-0005640.
XX PA (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
Telford J, Massignani V, Margarit Ros YI, Grandi G, Fraser C;
XX WPI; 2002-352536/38.
DR N-FSDB; ABN71085.
XX New Streptococcus protein for the treatment or prevention of infection
PT or disease caused by Streptococcus bacteria, such as meningitis, and
PT for detecting a compound that binds to the protein -
XX PS Claim 1: Page 4137; 4525pp; English.
CC The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus Pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. Pyogenes.
CC Nucleic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (I) may be used to recombinantly produce (I) and may be
CC used in gene therapy. Antibodies to (I) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins.
XX Sequence 187 AA;
XX Every Match 57.1%; Score 44; DB 23; Length 187;
XX best local similarity 75.0%; pred. no. 6.1;
XX Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX QY 5 SPRGVIASNLXF 16
XX Db 56 SPRGVIAKLVF 67
XX RESULT 8 ABP28247 standard; Protein; 230 AA.
XX ABP28247; AC ABP28247;
XX DT 02-JUL-2002 (first entry)
XX DE Streptococcus polypeptide SEQ ID NO 5670.
XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus Pyogenes; antibacterial; antiinflammatory;
KW infection; vaccine; meningitis; gene therapy.
XX OS XX Streptococcus agalactiae.
XX PN WO200234771-A2.
XX PD 02-MAY-2002.
XX PR 29-OCT-2001; 2001WO-GB04789.
XX PR 27-OCT-2000; 2000GB-0026333.
XX PR 24-NOV-2000; 2000GB-0028727.
XX PR 07-MAR-2001; 2001GB-0005640.

RESULT 7 ABY91319
ID ABY91319 standard; Protein; 230 AA.
AC ABY91319;
XX DT 30-MAY-2000 (first entry)
DB Group B Streptococcus protein sequence SEQ ID NO:47.
XX

XX
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 PT Telford J', Massignani V, Margarit Ros YI, Grandi G, Fraser C;
 PI Tettelein H;
 XX
 DR WPI: 2002-352536/38.
 DR N-PSDB; ASN68878.

XX
 PT New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
 XX
 Claim 1; Page 3729; 452PP; English.

The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/sBS (Streptococcus agalactiae) or group A streptococcus/gAS (Streptococcus Pyogenes), comprising one of 5483 sequences (SI), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S agalactiae and S. Pyogenes.

Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying Streptococcus proteins.

XX
 Sequence 230 AA;

Query Match 57.1%; Score 44; DB 23; Length 230;
 Best Local Similarity 75.0%; Pred. No. 7.7;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 5 SPRGVIASNLXF 16
 |||||||:|||
 Db 56 SPRGVIASNLXF 67

RESULT 9
 ID ABG07191 standard; Protein: 2506 AA.
 XX
 ABG07191;
 DT 13-FEB-2002 (first entry)
 XX
 Novel human diagnostic protein #7182.
 XX
 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
 KW Homo sapiens.
 OS Homo sapiens.
 XX
 WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PR 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649157.
 XX
 PR (HYSE-) HYSEQ INC.
 XX
 PI Demanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; ASN684251.

XX
 DR WPI: 2001-639362/73.
 DR N-PSDB; ASN1378.

XX
 PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
 XX
 PS Claim 20; SEQ ID No 37550; 103PP; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating or treating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/Pub/published_pct_sequences](http://wipo.int/Pub/published_pct_sequences).

XX
 Sequence 2506 AA;

Query Match 54.5%; Score 42; DB 22; Length 2506;
 Best Local Similarity 53.3%; Pred. No. 2.6e+02;
 Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 OY 2 LPMSPRGVIASNLXF 16
 ||| ||||: |||
 Db 745 LPAPPRGVVORRLTE 759

RESULT 10
 ID ABC30064 standard; Protein: 2506 AA.
 XX
 AC ABC30064;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 Novel human diagnostic protein #30055.
 XX
 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
 KW Homo sapiens.
 OS Homo sapiens.
 XX
 WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PR 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649157.
 XX
 PR (HYSE-) HYSEQ INC.
 XX
 PI Demanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.

KW allergic rhinitis; diabetes; multiple sclerosis; depression; disorder;
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
 XX neurological disorder.

OS Homo sapiens.

XX WO200153455-A2.

XX PN 26-JUL-2001.

XX PD 22-DEC-2000; 2000WO-US35017.

XX PR 23-DEC-1999; 99US-0471275.
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.

XX PA (HYSE-) HYSEQ INC.

XX PT Tang YT, Liu C, Dermanac RT;
 XX N-PSDB; ABK99543.
 WPI: 2001-457603/49.

PT Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
 PS claim 20; Page 230; 1217PP; English.

XX AAH99166 to AAH99904 encode the human proteins given in AMM25225 to AMM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; antimutagen; cardiovascular; antiangiogenesis; anti-HIV; fungicide; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g., inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and neurological disorders.

XX Sequence 1193 AA;

XX Query Match 51.9%; Score 40; DB 22; Length 1193;
 XX Best Local Similarity 43.8%; Pred. No. 2.6e+02;
 XX Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DLPMSPREVIASNLX 16
 ||| : ||| : |
 Db 1113 DLPLHPRGFLPGHAPP 1128

RESULT 15
 ABG61824 ABG61824 standard; Protein: 1193 AA.
 ID ABG61824;
 XX AC ABG61824;
 XX DT 15-AUG-2002 (first entry)
 XX DE Prostate cancer-associated protein #25.
 XX KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.

XX Sequence 1193 AA;

XX Query Match 51.9%; Score 40; DB 23; Length 1193;
 XX Best Local Similarity 43.8%; Pred. No. 2.6e+02;
 XX Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DLPMSPREVIASNLX 16
 ||| : ||| : |
 Db 1113 DLPLHPRGFLPGHAPP 1128

RESULT 16
 AAU32407 AAU32407 standard; Protein: 1194 AA.
 ID AAU32407
 XX AC AAU32407;
 XX DT 18-DEC-2001 (first entry)
 XX DE Novel human secreted protein #2898.
 XX KW Human; vaccination; gene therapy; nutritional supplement;
 XX KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO20017949-A2.
 XX
 PD 25-OCT-2001.
 XX
 PR 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 XX
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSE-) HYSEQ INC.
 Tang YT, Liu C, Dumanac RT;
 WPI; 2001-611725/70.

XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 XX
 PS Claim 20: Page 605-606; 765pp; English.

XX
 CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 PT determining the presence of or predisposition to a disease associated
 XX with altered levels of polypeptide. The polypeptides are also useful for
 PS identifying agents (agonists and antagonists) that bind to them. Cells
 XX expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation, to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration.
 CC Immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AU9510-AU3304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 XX
 SQ Sequence 1194 AA;

Query Match	51.9%	Score	40	DB	22	Length	1194
Best Local Similarity	43.8%	Pred. No.	2.6e+02				
Matches	7	Conservative	3	Mismatches	6	Indels	0
Qy	1 DLPMSPREVIAKX 16	Db	1114 DLPLHPRGFLPGHAPF 1129	SQ Sequence	70 AA:		

RESULT 17
 ABC24042
 ID ABC24042 standard; Protein: 70 AA.
 AC
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #24033.
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PR 30-MAR-2001; 2001WO-US08631.

XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649157.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Dumanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS88229.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID No 54401; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences AB60010-AB610377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 XX at ftp.wipo.int/pub/published_pct_sequences.

PR	31-JAN-2000;	2000US-0179065.	PR	02-OCT-2000;	2000US-0237037.
PR	04-FEB-2000;	2000US-0180628.	PR	02-OCT-2000;	2000US-0237038.
PR	24-FEB-2000;	2000US-0184664.	PR	02-OCT-2000;	2000US-0237039.
PR	02-MAR-2000;	2000US-0186350.	PR	02-OCT-2000;	2000US-023740.
PR	16-MAR-2000;	2000US-0189874.	PR	13-OCT-2000;	2000US-0239935.
PR	17-MAR-2000;	2000US-0190075.	PR	13-OCT-2000;	2000US-0239937.
PR	07-JUL-2000;	2000US-0198123.	PR	20-OCT-2000;	2000US-0240960.
PR	18-APR-2000;	2000US-0198123.	PR	20-OCT-2000;	2000US-0241221.
PR	19-MAY-2000;	2000US-0205515.	PR	20-OCT-2000;	2000US-0241785.
PR	17-JUN-2000;	2000US-0209467.	PR	20-OCT-2000;	2000US-0241787.
PR	28-JUN-2000;	2000US-0214886.	PR	20-OCT-2000;	2000US-0241808.
PR	30-JUN-2000;	2000US-0215135.	PR	20-OCT-2000;	2000US-0241809.
PR	07-JUL-2000;	2000US-0216647.	PR	20-OCT-2000;	2000US-0241826.
PR	11-JUL-2000;	2000US-0217487.	PR	01-NOV-2000;	2000US-0244617.
PR	11-JUL-2000;	2000US-0217496.	PR	08-NOV-2000;	2000US-0246474.
PR	14-JUL-2000;	2000US-0218290.	PR	08-NOV-2000;	2000US-0246475.
PR	26-JUL-2000;	2000US-0220963.	PR	08-NOV-2000;	2000US-0246476.
PR	26-JUL-2000;	2000US-0220964.	PR	08-NOV-2000;	2000US-0246477.
PR	14-AUG-2000;	2000US-0224518.	PR	08-NOV-2000;	2000US-0246478.
PR	14-AUG-2000;	2000US-0224519.	PR	08-NOV-2000;	2000US-0246523.
PR	14-AUG-2000;	2000US-0225213.	PR	08-NOV-2000;	2000US-0246524.
PR	14-AUG-2000;	2000US-0225214.	PR	08-NOV-2000;	2000US-0246525.
PR	14-AUG-2000;	2000US-0225266.	PR	08-NOV-2000;	2000US-0246526.
PR	14-AUG-2000;	2000US-0225267.	PR	08-NOV-2000;	2000US-0246527.
PR	14-AUG-2000;	2000US-0225268.	PR	08-NOV-2000;	2000US-0246528.
PR	14-AUG-2000;	2000US-0225270.	PR	08-NOV-2000;	2000US-0246532.
PR	14-AUG-2000;	2000US-0225447.	PR	08-NOV-2000;	2000US-0246609.
PR	14-AUG-2000;	2000US-0225557.	PR	08-NOV-2000;	2000US-0246610.
PR	14-AUG-2000;	2000US-0225758.	PR	08-NOV-2000;	2000US-0246611.
PR	14-AUG-2000;	2000US-0225759.	PR	08-NOV-2000;	2000US-0246613.
PR	18-AUG-2000;	2000US-0226279.	PR	17-NOV-2000;	2000US-0249207.
PR	22-AUG-2000;	2000US-0226661.	PR	17-NOV-2000;	2000US-0249208.
PR	22-AUG-2000;	2000US-0226868.	PR	17-NOV-2000;	2000US-0249209.
PR	22-AUG-2000;	2000US-0227182.	PR	17-NOV-2000;	2000US-0249210.
PR	23-AUG-2000;	2000US-0227009.	PR	17-NOV-2000;	2000US-0249211.
PR	30-AUG-2000;	2000US-0228924.	PR	17-NOV-2000;	2000US-0249212.
PR	01-SEP-2000;	2000US-0229437.	PR	17-NOV-2000;	2000US-0249213.
PR	01-SEP-2000;	2000US-022943.	PR	17-NOV-2000;	2000US-0249214.
PR	01-SEP-2000;	2000US-0229344.	PR	17-NOV-2000;	2000US-0249215.
PR	05-SEP-2000;	2000US-0229345.	PR	17-NOV-2000;	2000US-0249216.
PR	05-SEP-2000;	2000US-0229509.	PR	17-NOV-2000;	2000US-0249217.
PR	05-SEP-2000;	2000US-0229513.	PR	17-NOV-2000;	2000US-0249218.
PR	05-SEP-2000;	2000US-0230437.	PR	17-NOV-2000;	2000US-0249244.
PR	05-SEP-2000;	2000US-0230438.	PR	17-NOV-2000;	2000US-0249245.
PR	08-SEP-2000;	2000US-0231242.	PR	17-NOV-2000;	2000US-0249264.
PR	08-SEP-2000;	2000US-0231243.	PR	17-NOV-2000;	2000US-0249265.
PR	12-SEP-2000;	2000US-0231968.	PR	17-NOV-2000;	2000US-0249297.
PR	08-SEP-2000;	2000US-0231244.	PR	17-NOV-2000;	2000US-0249299.
PR	14-SEP-2000;	2000US-0231413.	PR	17-NOV-2000;	2000US-0249300.
PR	08-SEP-2000;	2000US-0231414.	PR	17-NOV-2000;	2000US-0249301.
PR	08-SEP-2000;	2000US-0232080.	PR	01-DEC-2000;	2000US-0250160.
PR	08-SEP-2000;	2000US-0232081.	PR	01-DEC-2000;	2000US-0250391.
PR	12-SEP-2000;	2000US-0233063.	PR	05-DEC-2000;	2000US-0251030.
PR	14-SEP-2000;	2000US-0233065.	PR	05-DEC-2000;	2000US-0251988.
PR	14-SEP-2000;	2000US-0233065.	PR	05-DEC-2000;	2000US-0251989.
PR	21-SEP-2000;	2000US-0233423.	PR	06-DEC-2000;	2000US-0251479.
PR	25-SEP-2000;	2000US-0234497.	PR	08-DEC-2000;	2000US-0251856.
PR	25-SEP-2000;	2000US-0234498.	PR	08-DEC-2000;	2000US-0251868.
PR	25-SEP-2000;	2000US-0235484.	PR	08-DEC-2000;	2000US-0251989.
PR	27-SEP-2000;	2000US-0235834.	PR	08-DEC-2000;	2000US-0251990.
PR	27-SEP-2000;	2000US-0235836.	PR	11-DEC-2000;	2000US-0254097.
PR	27-SEP-2000;	2000US-0236327.	PR	05-JAN-2001;	2001US-0259678.
PR	29-SEP-2000;	2000US-0236367.	XX	(HUMA-) HUMAN GENOME SCI INC.	
PR	29-SEP-2000;	2000US-0236368.	XX	Rosen CA, Barash SC, Ruben SM;	
PR	29-SEP-2000;	2000US-0236369.	XX	WPI; 2001-451929/48.	
PR	29-SEP-2000;	2000US-0236370.	XX	N-PSDB; AAS40102.	
PR	02-OCT-2000;	2000US-0236602.	PT	Isolated polypeptide for treating, preventing and/or prognosing cancer disorders related to the reproductive system including prostate cancer	

PS
 XX
 CC
 The invention relates to novel isolated human prostate cancer antigen polynucleotides (I) and polypeptides (II). (I) and (II) are useful for preventing, treating or ameliorating a medical condition when administered. (I), (II) and the antibody to (II) are useful for treating preventing and/or prognosis disorders related to the reproductive system including prostate cancers; urinary disorders e.g. chronic nephritis; and blood-related disorders e.g. thrombosis. (II) can be used for testing and detection e.g. as a chromosomal marker and in forensics. (I) and the anti-(II) antibody can be used in testing and detection in immunoassays. AU27702-AU22913 represent the human prostate cancer antigen amino acid sequences, and related amino acid sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at: ftp.wipo.int/pub/published/pct/sequences.

XX SQ Sequence 84 AA;

Query Match	Score	DB	Length	84;
Best Local Similarity	50.6%	Pred.	No:	20;
Matches	7;	Conservative	Mismatches	2;
			Indels	1;
OY	2	LPMSPRGVIA	11	;
Db	52	IPLSPRAGVIA	61	;

RESULT 19
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 ID AAM94707 standard; Protein: 84 AA.
 XX
 AC AAM94707;
 XX
 DR 21-NOV-2001 (first entry)
 XX
 DE Human reproductive system related antigen SEQ ID NO: 3365.
 KW Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy.
 XX
 OS HOMO sapiens.
 XX
 PN WO200155320-A2.
 02-AUG-2001.
 17-JAN-2001; 2001WO-US01339.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0188874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0191123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.

PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
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 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251855.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 PT Rosen CA, Barash SC, Ruben SM;
 XX WPT; 2001-465570-50.
 DR N PSDB; AAL00677.
 XX Isolated nucleic acid molecule encoding a reproductive system antigen -
 PT is used in preventing, treating or ameliorating a medical condition -
 PT
 Claim 11; SEQ ID NO 3365; 1297pp + Sequence Listing; English.

The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention.

XX Sequence 84 AA;

Query Match 50.6%; Score 39; DB 22; Length 84;
 Best Local Similarity 70.0%; Pred No. 20;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

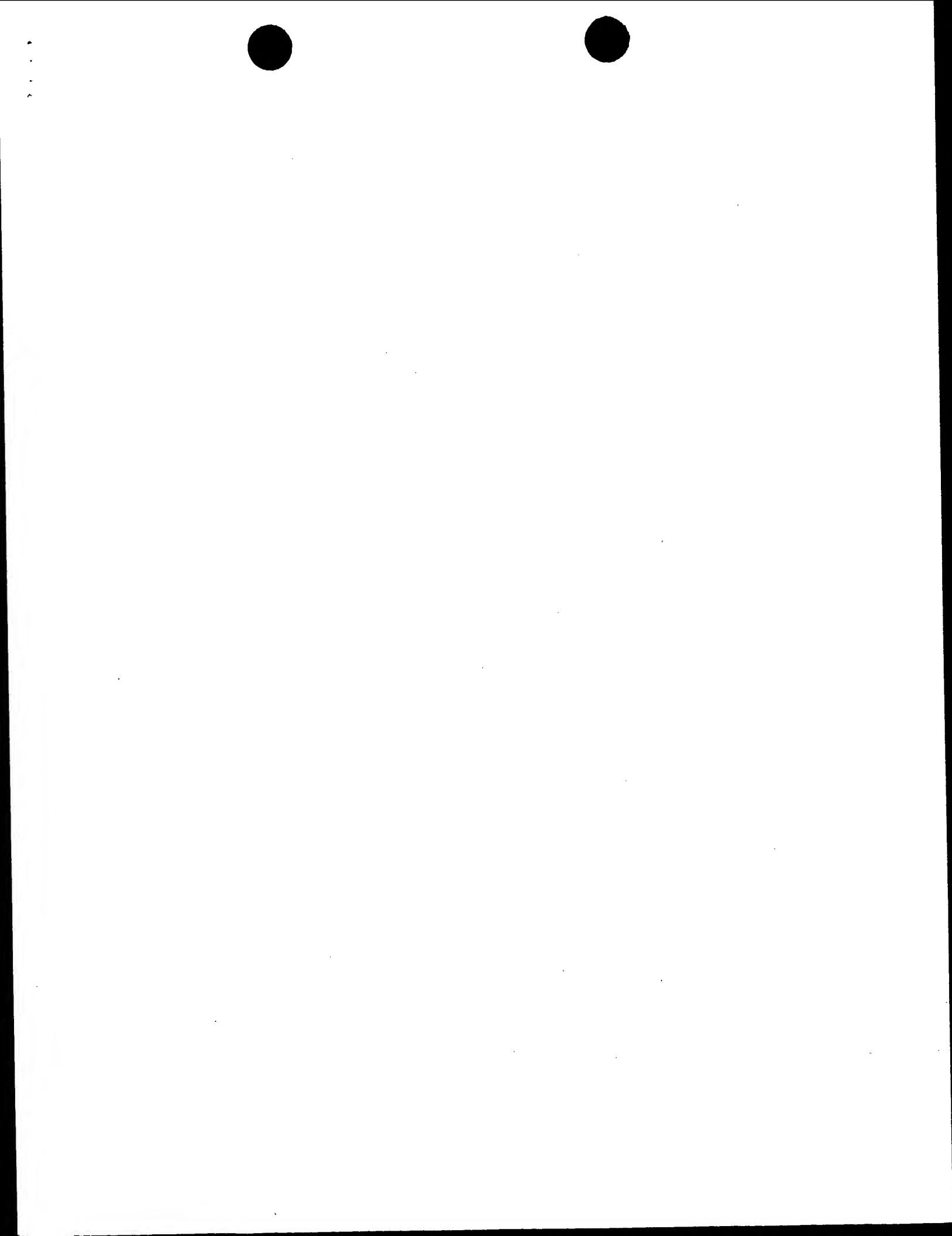
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 Db 52 IPLSPAGVIA 61

RESULT 20
 AAM89856 standard; Protein; 97 AA.
 ID AAM8986

XX
 AC AAM8986;
 XX
 DT 07-NOV-2001 (first entry)
 XX DE Human immune/haematopoietic antigen SEQ ID NO:17479.
 XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis.
 XX OS Homo sapiens.
 XX PN WO20015182-A2.
 XX PD 09-AUG-2001.
 XX PF 17-JAN-2001; 2001WO-US01354.
 XX PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
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 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
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 PR 14-AUG-2000; 2000US-0224518.
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 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-022557.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
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 PR 12-SEP-2000; 2000US-0231244.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.

PR 14-SEP-2000; 2000US-0233400. PR 06-DEC-2000; 2000US-0251479.
 PR 14-SEP-2000; 2000US-0233063. PR 08-DEC-2000; 2000US-0251856.
 PR 14-SEP-2000; 2000US-0233064. PR 08-DEC-2000; 2000US-0251868.
 PR 21-SEP-2000; 2000US-0234223. PR 08-DEC-2000; 2000US-0251989.
 PR 21-SEP-2000; 2000US-0234274. PR 08-DEC-2000; 2000US-0251990.
 PR 25-SEP-2000; 2000US-0234997. PR 11-DEC-2000; 2000US-0254097.
 PR 26-SEP-2000; 2000US-0235484. PR 05-JAN-2001; 2001US-0259678.
 PR 27-SEP-2000; 2000US-0235834. XX PA (HOMA-) HUMAN GENOME SCI INC.
 PR 27-SEP-2000; 2000US-0235835. XX PI Rosen CA, Barash SC, Ruben SM;
 PR 29-SEP-2000; 2000US-0236327. XX DR WPI; 2001-4834265/52.
 PR 29-SEP-2000; 2000US-0236368. XX N-PSDB; AAK62667.
 PR 29-SEP-2000; 2000US-0236369. XX
 PR 02-OCT-2000; 2000US-0236802. PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PR 02-OCT-2000; 2000US-0237037. PT useful for preventing, diagnosing and/or treating cancers and
 PR 02-OCT-2000; 2000US-0237038. PT metastasis
 PR 02-OCT-2000; 2000US-0237039. XX
 PR 13-OCT-2000; 2000US-0237040. RS Claim 11; SEQ ID NO 17479; 3071pp + Sequence Listing; English.
 PR 13-OCT-2000; 2000US-0239935. CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 PR 20-OCT-2000; 2000US-0239937. CC amino acid sequences given in AAM2170 to AAK9121. (I) have cytostatic
 PR 20-OCT-2000; 2000US-0241221. CC activity, and can be used in gene therapy and vaccine production. (I)
 PR 20-OCT-2000; 2000US-0241785. CC proteins and polynucleotides may be used in the prevention, diagnosis and
 PR 20-OCT-2000; 2000US-0241787. CC treatment of diseases associated with inappropriate (I) expression. For
 PR 20-OCT-2000; 2000US-0241809. CC example, they may be used to treat disorders associated with decreased
 PR 20-OCT-2000; 2000US-0241809. CC expression by rectifying mutations or deletions in a patient's genome
 PR 01-NOV-2000; 2000US-0241826. CC that affect the activity of (I), by expressing inactive proteins or to
 PR 08-NOV-2000; 2000US-0244617. CC supplement the patient's own production of (I). Additionally, (I)
 PR 08-NOV-2000; 2000US-0244647. CC polynucleotides may be used to produce the secreted (I) by inserting
 PR 08-NOV-2000; 2000US-0244675. CC the nucleic acids into a host cell and culturing the cell to express the
 PR 08-NOV-2000; 2000US-0246476. CC protein. (I) proteins and polynucleotides may be used to prevent,
 PR 08-NOV-2000; 2000US-0246477. CC diagnose and treat immune/hematopoietic-related diseases, especially
 PR 08-NOV-2000; 2000US-0246528. CC cancers and cancer metastases of haemopoietic-derived cells. AAK6794
 PR 08-NOV-2000; 2000US-0246532. CC to AAK8794 represent human immune/haematopoietic antigen genomic
 PR 08-NOV-2000; 2000US-0246533. CC sequences from the present invention. AAK5942 to AAK5490 and AAM2169
 PR 08-NOV-2000; 2000US-0246525. CC represent sequences used in the exemplification to the present invention.
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 PR 08-NOV-2000; 2000US-0246527. Sequence 97 AA;
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 PR 08-NOV-2000; 2000US-0246532. Best Local Similarity 70.0%; Pred. No. 23; Mismatches 0;
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 PR 08-NOV-2000; 2000US-0246611. DB 54 IPISPAGVIA 63
 PR 08-NOV-2000; 2000US-0246613. 17-NOV-2000; 2000US-0249307.
 PR 17-NOV-2000; 2000US-0249308. 17-NOV-2000; 2000US-0249314.
 PR 17-NOV-2000; 2000US-0249310. 17-NOV-2000; 2000US-0249311.
 PR 17-NOV-2000; 2000US-0249312. 17-NOV-2000; 2000US-0249313.
 PR 17-NOV-2000; 2000US-0249314. 17-NOV-2000; 2000US-0249315.
 PR 17-NOV-2000; 2000US-0249315. 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210. 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211. 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249217. 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218. 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249224. 17-NOV-2000; 2000US-0249224.
 PR 17-NOV-2000; 2000US-0249245. 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264. 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265. 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249275. 17-NOV-2000; 2000US-0249275.
 PR 17-NOV-2000; 2000US-0249299. 17-NOV-2000; 2000US-0249299.
 PR 01-DEC-2000; 2000US-0251160. 01-DEC-2000; 2000US-0251160.
 PR 01-DEC-2000; 2000US-0250391. 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030. 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988. 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.

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 Job time : 37 secs



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OM protein - protein search, using sw model

Run on: January 2, 2003, 12:03:04 ; Search time 34 seconds

(without alignments)
13.846 Million cell updates/sec

Title: US-09-824-053-3

Perfect score: 77 ; Sequence: 1 DLPMSPRGVIASNLXF 16

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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
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Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	75	97.4	546	4	US-08-669-304-31	Sequence 31, Appli
3	74	96.1	16	4	US-08-669-304-10	Sequence 10, Appli
4	39	50.6	468	4	US-09-282-097-2	Sequence 2, Appli
5	39	50.6	770	1	US-08-416-581B-1	Sequence 1, Appli
6	39	50.6	39	1	US-08-416-581B-5	Sequence 5, Appli
7	39	50.6	770	4	US-09-087-465-6	Sequence 6, Appli
8	39	50.6	771	1	US-08-286-098A-14	Sequence 14, Appli
9	39	50.6	771	1	US-08-781-890-14	Sequence 14, Appli
10	38	49.4	393	4	US-09-387-418A-10	Sequence 10, Appli
11	38	49.4	770	1	US-08-469-796-12	Sequence 12, Appli
12	38	49.4	770	1	US-08-416-581B-9	Sequence 9, Appli
13	38	49.4	770	2	US-08-852-091-12	Sequence 12, Appli
14	38	49.4	770	2	US-08-820-734-12	Sequence 12, Appli
15	38	49.4	770	3	US-09-556-622-12	Sequence 12, Appli
16	38	49.4	770	3	US-08-956-633A-12	Sequence 12, Appli
17	38	49.4	770	3	US-08-012-710-8	Sequence 8, Appli
18	38	49.4	770	3	US-08-948-577-12	Sequence 12, Appli
19	38	49.4	770	4	US-09-364-970-3	Sequence 3, Appli
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22	38	49.4	770	4	US-08-956-633A-12	Sequence 12, Appli
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24	38	49.4	770	5	PCT-US05-17025-12	Sequence 12, Appli
25	38	49.4	4544	1	US-08-669-416-52	Sequence 52, Appli
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27	37	48.1	307	4	US-08-558-207A-481	Sequence 481, Appli

RESULT 1
US-08-669-304-3
; Sequence 3, Application US/08669304
; Patent No. 6251626
GENERAL INFORMATION:
APPLICANT: Peter Stougaard
APPLICANT: Ole Cal Hansen
TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hunton & Williams
STREET: 1900 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006-1109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-669-304
FILING DATE: 12 July 1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/476,910
FILING DATE: 7 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: Stanislaus Aksman
REGISTRATION NUMBER: 28,562
REFERENCE/DOCKET NUMBER: 320.000003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 955-1926
TELEFAX: (202) 778-2201
TELEX: No. 6251626e
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-669-304-3

Query Match 97.4%; Score 75; DB 4; Length 16;
Best Local Similarity 100%; Pred. No. 3.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-08-669-304-31
Sequence 31, Application US/08669304
GENERAL INFORMATION:
PATENT NO.: 6251626
APPLICANT: Peter Stougaard
TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME
TITLE OF SEQUENCES: 34
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hunton & Williams
STREET: 1900 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006-1109
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, version #1.25
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,304
FILING DATE: 12 July 1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/476,910
FILING DATE: 7 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: Stanislav Aksman
REGISTRATION NUMBER: 28,562
REFERENCE/DOCKET NUMBER: 320.000003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 955-1926
TELEFAX: (202) 778-2201
TELEX: No. 6251626
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-669-304-31
Query Match 97.4%; Score 75; DB 4; Length 46;
Best Local Similarity 93.8%; Pred. No. 1.8e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 DLPMSPRGVIAISNLXF 16
||| ||| ||| ||| |||
Db 219 DLPMSPRGVIAISNLHF 234
RESULT 3
US-08-669-304-10
Sequence 10, Application US/08669304
GENERAL INFORMATION:
PATENT NO.: 6251626
APPLICANT: Peter Stougaard
TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hunton & Williams
STREET: 1900 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006-1109
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, version #1.25
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,304
FILING DATE: 12 July 1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/476,910
FILING DATE: 7 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: Stanislav Aksman
REGISTRATION NUMBER: 28,562
REFERENCE/DOCKET NUMBER: 320.000003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 955-1926
TELEFAX: (202) 778-2201
TELEX: No. 6251626
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-669-304-10
Query Match 96.1%; Score 74; DB 4; Length 16;
Best Local Similarity 93.8%; Pred. No. 4.9e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DLPMSPRGVIAISNLXF 16
Db 1 DLPMSPRGVIAISNLWF 16
RESULT 4
US-09-292-097-2
Sequence 2, Application US/09292097B
GENERAL INFORMATION:
PATENT NO.: 6322977
APPLICANT: Lal, Preeti
APPLICANT: Kaser, Matthew, R.
APPLICANT: Baughn, Mariah, R.
TITLE OF INVENTION: TAPIA-LIKE PROTEIN
FILE REFERENCE: PC-0002 US
CURRENT APPLICATION NUMBER: US/09/292,097B
CURRENT FILING DATE: 1999-04-14
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PERL Program
SEQ ID NO 2
LENGTH: 468
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: -
OTHER INFORMATION: 103348CD1
US-09-292-097-2
Query Match 50.6%; Score 39; DB 4; Length 468;
Best Local Similarity 31.5%; Pred. No. 39;
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
Qy 1 DLPMSPRGVIAISNLXF 16
Db 176 NLPLSPQGIVRTAVEF 191
RESULT 5

US-08-416-581B-1

Sequence 1, Application US/08416581B
 Patent No. 5719042
 GENERAL INFORMATION:
 APPLICANT: Kishimoto, Tadamitsu
 TITLE OF INVENTION: TRANSCRIPTION FACTOR APPF
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
 STREET: 2100 Pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20037

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/416,581B
 FILING DATE: 04-APR-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 6-05825/1994
 FILING DATE: 04-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Nakamura, Dean H.
 REGISTRATION NUMBER: 33,981
 REFERENCE/DOCKET NUMBER: Q-37891

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)293-7060
 TELEFAX: (202)293-7860

SEQUENCE CHARACTERISTICS:
 LENGTH: 770 amino acids

TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-416-581B-1

Query Match 50.6%; Score 39; DB 1; Length 770;
 Best Local Similarity 77.8%; Pred. No. 70;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 DLPMSPRGV 9
 111111 :
 723 DLPMSPRAL 731

RESULT 6

US-08-416-581B-5

; Sequence 5, Application US/08416581B
 ; Patent No. 5719042
 ; GENERAL INFORMATION:
 ; APPLICANT: Kishimoto, Tadamitsu
 ; APPLICANT: Akira, Shizuo
 ; TITLE OF INVENTION: TRANSCRIPTION FACTOR APPF
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
 ; STREET: 2100 Pennsylvania Avenue, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20037

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

RESULT 7

US-09-087-465-6

; Sequence 6, Application US/09087465A
 ; Patent No. 616092
 ; GENERAL INFORMATION:
 ; APPLICANT: Vinkemeier, Uwe
 ; APPLICANT: Chen, Xiaomin
 ; APPLICANT: Darrell Jr., James E
 ; APPLICANT: Kurlyan, John
 ; TITLE OF INVENTION: A CRYSTAL OF THE CORE PORTION OF A STAT AND METHODS OF
 ; FILE REFERENCE: 600-1-29
 ; CURRENT APPLICATION NUMBER: US/09/087,465A
 ; CURRENT FILING DATE: 1998-05-29
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 770
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-087-465-6

Query Match 50.6%; Score 39; DB 4; Length 770;
 Best Local Similarity 77.8%; Pred. No. 70;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLPMSPRGV 9
 Db 723 DLPMSPRAL 731

RESULT 8

US-08-276-099A-14

; Sequence 14, Application US/08276099A
 ; Patent No. 5591825
 ; GENERAL INFORMATION:
 ; APPLICANT: McRight, Steven L
 ; APPLICANT: Hou, Jinzhao
 ; TITLE OF INVENTION: INTERLEUKIN-4 SIGNAL TRANSDUCERS AND
 ; TITLE OF INVENTION: BINDING ASSAYS
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/369,796

FILING DATE: 06-JAN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-116

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 133521 343-1684

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 770 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-369-796-12

Query Match 49.4%; Score 38; DB 1; Length 770;

Best Local Similarity 100.0%; Pred. No. 1e+02; 0; Indels

Matches 7; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 DLPMSPR 7

Db 723 DLPMSPR 729

RESULT 13

US-08-852-091-12

Sequence 12, Application US/08852091

Patent No. 5833228

GENERAL INFORMATION:

APPLICANT: James E. Darnell, Jr.

APPLICANT: Zilong Wen

APPLICANT: Curt M. Horvath

APPLICANT: Zhong Zhong

TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/852,091

FILING DATE: 06-MAY-1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/369,796

FILING DATE: 06-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-116

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 133521 343-1684

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 770 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-852-091-12

Query Match 49.4%; Score 38; DB 2; Length 770;

Best Local Similarity 100.0%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 DLPMSPR 7

Db 723 DLPMSPR 729

RESULT 14

US-08-820-754-12

Sequence 12, Application US/08820754

Patent No. 5976835

ATTORNEY/AGENT INFORMATION:

NAME: Nakamura, Dean H.

REGISTRATION NUMBER: 33,981

REFERENCE/DOCKET NUMBER: Q-37891

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)293-7860

TELEFAX: (202)293-7860

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 770 amino acids

TYPE: amino acid

GENERAL INFORMATION:

APPLICANT: Darnell Jr., James E.

APPLICANT: Schindler, Christian W.

APPLICANT: Wen, Zilong

APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN SEQUENCES AND METHODS OF USE THEREOF

TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/820,754

FILING DATE: 19-MAR-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/212,185

FILING DATE: 11-MAR-1994

APPLICATION NUMBER: US 07/980,498

FILING DATE: 23-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/654,296

FILING DATE: 19-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO US93/02569

FILING DATE: 19-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/126,588

FILING DATE: 24-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-073 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 770 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

820-754-12

Query Match 49.4%; Score 38; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLPMSPR 7

Db 723 DLPMSPR 729

RESULT 15
US-08-956-652-12 Application US/08956652
Sequence 12 Application US/08956869
Patient No. 6030808
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
APPLICANT: Receptor Recognition Factors, Protein Sequences and Methods of Use Thereof
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:RESULT 16
US-08-956-869-12
Sequence 12 Application US/08956869
Patient No. 6030808
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
APPLICANT: Receptor Recognition Factors, Protein Sequences and Methods of Use Thereof
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:

FILING DATE: 19-MAR-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 09/125, 588
 FILING DATE: 24-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-073 CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 343-1684
 TELEX: 13521
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 770 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ; US-09-948-547-12

Query Match 49.4%; Score 38; DB 3; Length 770;
 Best Local Similarity 100.0%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

Qy	1 DLPMSPR 7 	Db	723 DLPMSPR 729

RESULT 19

US-09-364-970-3

; Sequence 3, Application US/09364970

; Patent No. 6235873

; GENERAL INFORMATION:

; APPLICANT: Bromberg, Jacqueline
 TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR

USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING

TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING

TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES

FILE REFERENCE: 600-1-252

CURRENT APPLICATION NUMBER: US/09/364, 970

CURRENT FILING DATE: 1999-07-31

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 770
 TYPE: PRT
 ORGANISM: Mus musculus

US-09-364-970-3

Query Match 49.4%; Score 38; DB 4; Length 770;
 Best Local Similarity 100.0%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

Qy	1 DLPMSPR 7 	Db	723 DLPMSPR 729

RESULT 20

US-09-364-970-5
 Sequence 5, Application US/09364970

; Patent No. 6235873

; GENERAL INFORMATION:

; APPLICANT: Bromberg, Jacqueline

; TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR

USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING

TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES

FILE REFERENCE: 600-1-252

CURRENT APPLICATION NUMBER: US/09/364, 970

CURRENT FILING DATE: 1999-07-31

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5

LENGTH: 770
 TYPE: PRT
 ORGANISM: Mus musculus

US-09-364-970-5

Query Match 49.4%; Score 38; DB 4; length 770;
 Best Local Similarity 100.0%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

Qy	1 DLPMSPR 7 	Db	723 DLPMSPR 729

Search completed: January 2, 2003, 12:05:31
 Job time : 36 secs

GenCore - version 5.1.3
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OM protein - protein search, using sw model

Run on: January 2, 2003, 12:03:04 ; Search time 16 Seconds
(without alignments)
96.134 Million cell updates/sec

Title: US-09-824-053-3
Perfect score: 77
Sequence: DLPMSPRGVIASNLXF 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_73;*

1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	43	55.8	184	E98229	sarcosine oxidase
2	43	55.8	184	A13056	sarcosine oxidase
3	42	54.5	416	B65171	hypothetical prote
4	41	53.2	416	E91207	hypothetical prote
5	41	53.2	416	G86053	hypothetical prote
6	40	51.9	295	A60131	homocytic protein X
7	40	51.9	407	G84309	hypothetical prote
8	39	50.6	113	2	transcription fact
9	39	50.6	113	2	hypothetical prote
10	39	50.6	770	2	DNA-binding prote
11	38	49.4	272	1	ribonuclease hom
12	38	49.4	328	2	conserved hypothet
13	38	49.4	334	2	glycerol-3-P dehyd
14	38	49.4	334	2	glycerol-3-phospho
15	38	49.4	363	2	hypothetical prote
16	38	49.4	479	2	hypothetical prote
17	38	49.4	670	2	conserved hypothet
18	38	49.4	684	2	hypothetical prote
19	38	49.4	770	2	ISGF3 P91-related
20	38	49.4	1305	2	cyclin G-associate
21	38	49.4	4543	1	alpha-2-macroglobu
22	38	49.4	4544	1	alpha-2-macroglobu
23	38	49.4	4545	1	alpha-2-macroglobu
24	37	48.1	196	2	MADS box protein F
25	37	48.1	245	2	hypothetical prote
26	37	48.1	362	2	P43 orf39 - Bombyx
27	37	48.1	368	2	conserved hypothet
28	37	48.1	485	1	probable periplasm
29	37	48.1	500	2	hypothetical prote

30 37 48.1 605 2 139837
31 37 48.1 607 2 B86744
32 37 48.1 607 2 S39342
33 37 48.1 607 2 B95060
34 37 48.1 607 2 G97280
35 37 48.1 611 2 S09500
36 37 48.1 614 2 B83818
37 37 48.1 631 2 S71508
38 37 48.1 637 2 B83052
39 37 48.1 749 2 A99338
40 37 48.1 860 2 A43920
41 37 48.1 861 2 G02329
42 37 48.1 885 2 JH0796
43 37 48.1 1199 2 S76349
44 37 48.1 1477 2 T18534
45 37 48.1 2218 2 B84683

ALIGMENTS

dikak-type molecule
dikak protein lmpo
dikak-type molecule
hypothetical prote
hypothetical prote
dikak-type molecule
class I heat-shock
dikak-type molecule
Dikak protein PA476
hypothetical prote
nucleolar 100K pol
replication contr
nucleolar 100K pol
transcription-repa
protein-tyrosine k
hypothetical prote

RESULT 1
E98229
sarcosine oxidase gamma chain PA5419 [imported] - Agrobacterium tumefaciens (strain C
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C;Accession: E98229
R;Goodner, B.; Hinkie, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm
A.; Liu, F.; Wollan, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A;Reference number: A97359; PMID:11743194
A;Accession: E98229
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-184 <KUR>
A;Cross-references: GB;AE007870; PIDN:AK89359.1; PID:915159207; GSPDB:GN00170
A;Gene: AGRL_1572
A;Map position: linear chromosome
C;Superfamily: Corynebacterium sp. sarcosine oxidase gamma chain
C;Genetics:

Query	Match	Best Local Similarity	Score	DB	Length
QY	2	LPMSPRGVIASNLXF 16	55.8%	2	184
Db	54	LPTSPKGSVNSGLRF 68	53.3%	2	184

RESULT 2
A13056
sarcosine oxidase gamma subunit [imported] - Agrobacterium tumefaciens (strain C58, D
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C;Accession: A13056
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCle
;Karp, P.; Romero, P.; Zhang, S.
Science 294, 2171-2223, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: A13056
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-184 <KUR>
A;Cross-references: PIDN:AA144871.1; PID:917742519; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: soxG

A; Map position: linear chromosome
C; Superfamily: Corynebacterium sp. sarcosine oxidase gamma chain

B6571

hypothetical protein yidR - Escherichia coli (strain K-12)

Query Match Score 43; DB 2; Length 184;

Best Local Similarity 55.8%; Pred. No. 3.2;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY ||||| : | | |
OY ||| | | : | | |

Db 54 LPTSPKGSVnSGLRF 68

RESULT 3

B6571

hypothetical protein yidR - Escherichia coli (strain K-12)

Query Match Score 43; DB 2; Length 184;

Best Local Similarity 53.3%; Pred. No. 3.2;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 LPMSPPRGVIAASNLXF 16

Db 54 LPTSPKGSVnSGLRF 68

RESULT 4

B6571

hypothetical protein yidR - Escherichia coli (strain K-12)

Query Match Score 43; DB 2; Length 184;

Best Local Similarity 53.2%; Pred. No. 3.2;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY ||| | | : | | |
OY ||| | | : | | |

Db 272 LPAPPRGIVQRRLTF 286

RESULT 5

B6571

hypothetical protein yidR - Escherichia coli (strain K-12)

Query Match Score 43; DB 2; Length 184;

Best Local Similarity 53.3%; Pred. No. 3.2;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY ||| | | : | | |
OY ||| | | : | | |

Db 272 LPAPPRGIVQRRLTF 286

G86053 hypothetical protein yidR [imported] - Escherichia coli (strain 0157:H7, substrain ED hypothetical protein yidR [imported] - Escherichia coli (strain 0157:H7, substrain ED

C; Species: Escherichia coli C; Species: Escherichia coli

C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C; Accession: G86053 C; Accession: G86053

R; Perna, N.T.; Blunckett III, G.; Burland, V.; Mau, B.; Glaser, J.D.; Rose, D.J.; May

iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimaranta, E.; Potamouisis, K.; Apoda

Nature 409, 529-533, 2001

A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A; Reference number: A85480; MUID:21074935; PMID:11206551

A; Accession: G86053 A; Accession: G86053

A; Status: preliminary A; Status: preliminary

A; Residues: 1-416 <SIO> A; Residues: 1-416 <SIO>

A; Cross-references: GB:BA00007; PIDN:BAB38052_1; PIDN:g13364104; GSPDB:GN00154; UWGP: A; Experimental source: strain 0157:H7, substrain EDL933

C; Genetics: C; Genetics:

A; Gene: yidR A; Gene: yidR

C; Superfamily: Escherichia coli hypothetical protein yidR C; Superfamily: Escherichia coli hypothetical protein yidR

Query Match Score 41; DB 2; Length 416; Query Match Score 41; DB 2; Length 416;

Best Local Similarity 53.2%; Pred. No. 18; Best Local Similarity 46.7%; Pred. No. 18;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 LPMSPPRGVIAASNLXF 16

Db 272 LPAPPRGIVQRRLTF 286

RESULT 6

A60131 hypothetical protein XHOX-7.1 - African clawed frog (fragment)

C; Species: Xenopus laevis (African clawed frog) C; Species: Xenopus laevis (African clawed frog)

C; Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 24-Sep-1999

C; Accession: A60131; S4513 C; Accession: A60131; S4513

R; Su, M.W.; Suzuki, R.H.; Solursh, M.; Ramirez, F. Development 111, 1179-1187, 1991

A; Title: Progressively restricted expression of a new homeobox-containing gene during

A; Reference number: A60131; MUID:91347929; PMID:1679007

A; Accession: A60131 A; Accession: A60131

A; Status: nucleic acid sequence not shown A; Status: nucleic acid sequence not shown

A; Molecule type: mRNA A; Molecule type: mRNA

A; Residues: 2-295 <SU4> A; Residues: 2-295 <SU4>

R; Su, M.W.; Suzuki, R.H.; Solursh, M.; Ramirez, F. submitted to the EMBL Data Library, December 1990

A; Reference number: S14513 A; Reference number: S14513

A; Accession: S14513 A; Accession: S14513

A; Molecule type: mRNA A; Molecule type: mRNA

A; Residues: 1-295 <SU4> A; Residues: 1-295 <SU4>

A; Cross-references: EMBL:X58773; PIDN:CAA41574_1; PIDN:g64783

C; Superfamily: unassigned homeobox proteins; homeobox homology

F;171-227/Domain: homeobox homology <HOX>

A; Gene: ECs4629 A; Gene: ECs4629

C; Genetics: C; Genetics:

A; Superfamily: Escherichia coli hypothetical protein yidR A; Superfamily: Escherichia coli hypothetical protein yidR

Query Match Score 41; DB 2; Length 416; Query Match Score 40; DB 2; Length 295;

Best Local Similarity 53.2%; Pred. No. 18; Best Local Similarity 46.7%; Pred. No. 19;

Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 LPMSPPRGVIAASNLXF 16

Db 272 LPAPPRGIVQRRLTF 286

RESULT 7

G84309 hypothetical protein Yngl1564h [imported] - Halobacterium sp. NRC-1

C; Species: Halobacterium sp. NRC-1 C; Species: Halobacterium sp. NRC-1

C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C; Accession: G84309 C; Accession: G84309

R; Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky

; Leithauer, B.; Keller, K.; Cruz, R.; Benson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja

RESULT 5

A; *LOC:* NALL; *Acad_Sci_U.S.A.* 97; *12116-12181*; *2000*
A; Authors: Hou, S.; Daniels, C.J.; Deinns, P.C.; Omer, A.D.; Ebhardt, H.; Lowe
A; Title: Genome sequence of *Halobacterium* species NRC-1.
A; Reference number: A04160; *Muid:* 20504483; *PMID:* 11016950
A; Accession: GB:J309
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-407 <STO>
A; Cross-references: GB:AE004437; NID:910581047; PIDN:AAG19843.1; GSPDB:GN00138
C; Genetics:
A; Gene: VNG1564H

Query	Match	Score	DB	Length
Best	Local Similarity	46.2%	Pred.	22
Matches			No.	407
1	DLPMSRGVIAVN	13	6;	Mismatches
223	DVALTPRGVVAAS	235	1:	Indels
	:	0;	Gaps	0.

```

C;Species : Homo Sapiens (man)
C;Name : APRF, p91, IFN-gamma, IFN-gamma, p91-related protein
C;Date : 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 28-Jul-2000
C;Accession : A54444
R;Akira, S.; Nisio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.:
Cell 77, 63-71, 1994
A;Title : Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related
A;Reference number : A54444; MUID:94208062; PMID:7512451
A;Accession : A54444

```

transcription factor - eastern newt (fragment)
 C;Species: *Nothophthalmus viridescens*, *Triturus viridescens* (eastern newt)
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Sep-1999
 C;Accession: I15025
 R;Simon, H.G.; Nelson, C.; Goff, D.; Laufer, E.; Morgan, B.A.; Tabin, C.
 Dev. Dyn. 202, 1-12, 1995
 A;Title: Differential expression of myogenic regulatory genes and Msx-1 during dedifferentiation
 A;Reference number: I15024; MUID:95218226; PMID:7703517
 A;Accession: I151025
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-113 <SIM>
 A;Cross-references: EMBL:X82837; NID:9577786; PIDN:CAA58044.1; PID:9577787
 A;Gene: Msx-1
 A;C;Genetics:
 C;Superfamily: unassigned homeobox proteins; homeobox homology
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F1;I-45/Domain: homeobox homology (fragment) <HOX>

A;Cross-references: GB:L29277; NID:9475788; PID:9475789
 C;Genetics:
 A;Gene: GDB:STAT3; APRF
 A;Cross-references: GDB:358950
 A;Map Position: 17q21-17q21
 C;Superfamily: human signal transducer and transcription activator STAT5A
 C;Keywords: DNA binding; transcription factor

Query Match
 Best Local Similarity 50.6%; Score 39; DB 2; Length 770;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DLPMSPRGV 9
 ||||| ;
 Db 723 DLPMSPRAL 731

RESULT 11
C64009
ribonuclease homolog HI0526 - *Haemophilus influenzae* (strain Rd KW20)
C;Species: *Haemophilus influenzae*
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 10-Sep-1999

hypothetical protein MJ0312 - Methanococcus jannaschii
Species: Methanococcus jannaschii
TaxID: 133996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
Accession: A64339
RI: Built; C.I.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.; Reich, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Carlson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Acuña, J.; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii; Reference number: A64300; MURID:96337999; PMID:8688087
Status: A64339
Molecule type: nucleic acid sequence not shown; translation not shown

A;Accession: C64009
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;residues: 1-272 <TIGR>
 A;Cross References: GB:J32735; GB:L42033; NID:9173509; PID: AAC22192.1; PID:91573510
 C;Superfamily: Enterobacter ribonuclease

Query	Match	Score	DB	Length
Qy	Best local similarity	49.4%	1	272
	Matches	50.0%	Pred. No.	39
Db	7; Conservative	3;	Mismatches	4
	: ; :		Indels	0
	170 DLPMSPRVIAASNL 14		Gaps	0

Cross-references: GB:U67486; GB:L77117; NID:91591031; PIDN:AA98309
Genetics:
Map Position: REV291845-291225

C;Accession: E95421
 R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
 ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
 Prod. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A;Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti*
 A;Reference number: A95262; MUID:21396509; PMID:11481432
 A;Accession: E95421
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-328 <KUR>
 A;Cross-references: GB:AE006469; PIDN:AAK65935.1; PID:914524450; GSPDB:GN00165
 A;Experimental source: strain 1021, megaplasmid pSymA
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puillier, A.; Abola, P.; Anupe, F.; Barloy-Hubler,
 R.; Galibert, F.; Finan, T.M.; Long, S.R.; Puillier, A.; Abola, P.; Anupe, F.; Barloy-Hubler,
 R.; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey
 L.; Hyman, R.W.; Jones, T.; Coddon, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe
 Science 293, 668-672, 2001
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 heault, P.; Vandenoever, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A;Reference number: A96039; MUID:21368234; PMID:11474104
 A;Genetics:
 A;Note: annotation
 A;Gene: gpaB; CP1014
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-334 <ARR>
 A;Cross-references: GB:AE002258; GB:AE002161; NID:97189919; PIDN:AAF38792.1; PID:9718
 A;Experimental source: strain AR39, HL cells
 A;Accession: D81513
 A;Reference number: A81500; MUID:20150255; PMID:10684935
 A;Gene: gpaB; CP1014
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-334 <ARR>
 A;Cross-references: GB:AE002258; GB:AE002161; NID:97189919; PIDN:AAF38792.1; PID:9718
 A;Experimental source: strain AR39, HL cells
 A;Accession: D81513
 A;Reference number: A81500; MUID:20150255; PMID:10684935
 QY 1 DLPMSPRGVIAASNL 14
 ||| ||| ||| :||| |
 Db 4 DIMMRNNVLASGL 17
 RESULT 13
 Query Match 49.4%; Score 38; DB 2; Length 328;
 Best Local Similarity 64.3%; Pred. No. 49; Mismatches 1; Indels 0; Gaps 0;
 Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 3 PMSPRGVIAASNLXF 16
 ||:||| ||| ||| |
 Db 48 PLAPNVVVISPNLSE 61
 RESULT 14
 Glycerol-3-P dehydrogenase [imported] - *Chlamydophila pneumoniae* (strain J138)
 C;Species: *Chlamydophila pneumoniae*, *Chlamydia pneumoniae*
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
 C;Accession: E85597
 C;Title: Comparison of whole genome sequences of *chlamydia pneumoniae* J138.
 R;Shirai, M.; Hirakawa, H.; Kinoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
 Nucleic Acids Res. 28, 2311-2314, 2000
 R;Title: Comparison of whole genome sequences of *chlamydia pneumoniae* J138.
 A;Title: Comparison of whole genome sequences of *chlamydia pneumoniae* J138.
 A;Reference number: A86491; MUID:20330349; PMID:10871362
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-334 <STO>
 A;Cross-references: GB:BA000008; NID:98979229; PIDN:BA9063.1; GSPDB:GN00142
 A;Experimental source: strain J138
 A;Genetics:
 C;Gene: gpda
 C;Name: gpda
 C;Family: glycerol-3-phosphate dehydrogenase
 C;Match 49.4%; Score 38; DB 2; Length 334;
 Best Local Similarity 50.0%; Pred. No. 50; Mismatches 7; Indels 4; Gaps 0;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 3 PMSPRGVIAASNLXF 16
 ||:||| ||| :||| |
 Db 48 PLAPNVVVISPNLSE 61
 RESULT 14
 GT2024
 glycerol-3-phosphate dehydrogenase, NAD-dependent CPO1014 [imported] - *Chlamydophila pneu*
 C;Species: *Chlamydophila pneumoniae*, *Chlamydia pneumoniae*
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
 C;Accession: G72024; D83513
 R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grinwood, J.;
 Nature Genet. 21, 385-399, 1999
 A;Title: Comparative genomes of *chlamydia pneumoniae* and *C. trachomatis*.
 A;Reference number: A72000; MUID:99206506; PMID:10193388
 A;Accession: G72024
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-334 <ARR>
 A;Cross-references: GB:AB001667; GB:AE001363; NID:94377171; PIDN:AAD1893.1; PID:9437
 A;Experimental source: strain CWL029
 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey
 C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe
 Nucleic Acids Res. 28, 1397-1406, 2000
 A;Title: Genome sequences of *Chlamydia trachomatis* MoPn and *Chlamydia pneumoniae* AR39
 A;Reference number: A81500; MUID:20150255; PMID:10684935
 A;Gene: gpaB; CP1014
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-334 <ARR>
 A;Cross-references: GB:AE002258; GB:AE002161; NID:97189919; PIDN:AAF38792.1; PID:9718
 A;Experimental source: strain AR39, HL cells
 A;Accession: D81513
 A;Reference number: A81500; MUID:20150255; PMID:10684935
 QY 3 PMSPRGVIAASNLXF 16
 ||:||| ||| |
 Db 48 PLAPNVVVISPNLSE 61
 RESULT 15
 Hypothetical protein - *Autographa californica* nuclear polyhedrosis virus
 C;Species: *Autographa californica* nuclear polyhedrosis virus, AcMNPV
 C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 21-Jul-2000
 C;Accession: G72854; A45684
 R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
 Virology 202, 586-605, 1994
 A;Title: The complete DNA sequence of *Autographa californica* nuclear polyhedrosis vir
 A;Reference number: A72850; MUID:94303173; PMID:8030224
 A;Accession: G72854
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-363 <AYR>
 A;Cross-references: GB:1-122858; NID:9510708; PIDN:AA66669.1; PID:9559108
 R;Carstens, E.B.; Lu, A.L.; Chan, H.L.
 J. Virol. 67, 2511-2520, 1993
 A;Title: Sequence, transcriptional mapping, and overexpression of p47, a baculovirus
 A;Reference number: A45684; MUID:93233214; PMID:8474157
 A;Accession: A45684
 A;Status: preliminary
 A;Molecule type: nucleic acid
 A;Residues: 1-363 <CAR>
 A;Cross-references: GB:1-107878; NID:9293990; PIDN:AAA16858.1; PID:9293991
 A;Note: sequence extracted from NCBI backbone (NCBIN:129587, NCBIPI:129588)
 C;Genetics:
 A;Gene: Acc-p43
 QY 2 LPMSPRGVIAASNLXF 16
 ||:||| :||| |
 Db 183 MPVKKKGVVSKNYAF 197
 RESULT 16
 S72582
 hypothetical protein B1937_C3_231 - *Mycobacterium leprae*
 C;Species: *Mycobacterium leprae*
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 22-Oct-1999

C;Accession: S72582
 R;Smith, D.R.; Robison, K.
 submitted to the EMBL Data Library, November 1993
 A;Reference number: S72580
 A;Accession: S72582
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-419 <SMT>
 A;Cross-references: EMBL:U00016; NID:9466961; PIDN:AAA17150.1; PID:9466964
 C;Genetics:
 A;Start codon: GTG

RESULT 17
 A75542
 Query Match 49.4%; Score 38; DB 2; Length 479;
 Best Local Similarity 70.0%; Pred. No. 75;
 Matches 7; Conservative 1; Mismatches 2;
 QY ||| :|||
 2 LPMSRGVIA 11
 225 LPMSRGVAA 234

RESULT 18
 A75542
 保守 hypothetical protein - *Deinococcus radiodurans* (strain R1)
 C;Species: *Deinococcus radiodurans*
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C;Accession: A75542
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.M.; Shem, M.; Vaithyanathan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Salawski, C.; Ma,
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A;Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A;Reference number: A75250; MUID:2036896; PMID:10567266
 A;Accession: A75542
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-670 <WHI>
 A;Cross-references: GB:AE001886; GB:AE000513; NID:96457921; PIDN:AAF09837.1; PID:9645792
 C;Experimental source: strain R1
 C;Genetics:
 A;Gene: DR0250
 A;Map position: 1

Query Match 49.4%; Score 38; DB 2; Length 670;
 Best Local Similarity 58.3%; Pred. No. 1.1e+02; Matches 7; Conservative 3; Mismatches 2;
 QY ||| :||| :|||
 5 SPRGVIASNLXF 16
 555 TPAGVVASSLF 566

RESULT 19
 A75542
 Query Match 49.4%; Score 38; DB 2; Length 684;
 Best Local Similarity 66.7%; Pred. No. 1.1e+02; Matches 6; Conservative 2; Mismatches 1;
 QY ||| :|||
 Db 176 PMEPKGIA 114

RESULT 20
 T31096
 Cyclin G-associated kinase GAK - rat
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 22-Oct-1999 #sequence_revision 22-oct-1999 #text_change 21-Jul-2000
 C;Accession: G90473
 C;Species: *Sulfolobus solfataricus*
 C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-Aug-2001
 C;Accession: G90473
 R;She, Q.; Singh, R.K.; Conflalonier, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan,
 Jong, I.; Jeffries, A.C.; Koza, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Reeder, F.,
 arrett, R.A.; Rogan, M.A.; Sensen, C.W.; Van der Oost, J.
 submitted to Geobank April 2001
 A;Description: *Sulfolobus solfataricus* complete genome.
 A;Reference number: A99139
 A;Accession: G90473
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-634 <KUR>
 A;Cross-references: GB:AEO06641; NID:913816315; PIDN:AAK43046.1; GSPDB:GN00155
 C;Genetics:
 C;Gene: cutA-6
 C;Superfamily: carbon-monoxide dehydrogenase large chain

Query Match 49.4%; Score 38; DB 2; Length 1305;
 Best Local Similarity 61.5%; Pred. No. 2.3e+02; Matches 8; Conservative 1; Mismatches 4;
 QY ||| :||| :|||
 Db 1015 DPAPENPKVISS 1027

Thu Jan 2 12:35:48 2003

us-09-824-053-3.rpr

Page 6

Search completed: January 2, 2003, 12:04:49
Job time : 18 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 2, 2003, 12:03:00 ; Search time 32 Seconds

(without alignments)
20.738 Million cell updates/sec

Title: US-09-824-053-3
Perfect score: 77
Sequence: 1 DLPMSPRGVIASNLXF 16

Using table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Defined:

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	42	54.5	416	1 YIDR_ECOLI	P31455 escherichia
2	40	51.9	295	1 HX7L_XENLA	004281 xenopus lae
3	39	50.6	206	1 Y312_MEWA	057763 methanococc
4	39	50.6	770	1 STX3_HUMAN	040763 homo sapien
5	38	49.4	272	1 RN26_HAIEIN	P44012 haemophilus
6	38	49.4	334	1 GPPA_CHIPN	092755 chlamydia p
7	38	49.4	363	1 VP43_NPAC	P34050 autographa
8	38	49.4	590	1 DNAK_STRAU	006942 streptococc
9	38	49.4	770	1 STX3_RAT	P42277 mus musculus
10	38	49.4	1305	1 GAK_RAT	P52631 rattus norvegicus;
11	38	49.4	4543	1 LREPL_CHICK	P97874 rattus norvegicus;
12	38	49.4	4544	1 LRR1_HUMAN	P98157 gallus gallus
13	38	48.1	1 FLC_ARATH	Q07954 homo sapien	
14	37	48.1	196	1 GAK_MOUSE	Q9s7q7 arabidopsis
15	37	48.1	499	1 GAK_MOUSE	Q99kya mus musculus
16	37	48.1	500	1 GGGS_PSEAG	Q93jy3 pseudomonas
17	37	48.1	604	1 DNAK_BACME	P05646 bacillus me
18	37	48.1	605	1 DNAK_BACTM	Q9kw57 bacillus th
19	37	48.1	607	1 DNAK_LACLA	P42368 lactococcus
20	37	48.1	607	1 DNAK_STREN	P95829 streptococc
21	37	48.1	607	1 DNAK_STREP	P95831 streptococc
22	37	48.1	609	1 DNAK_STRAG	P95693 streptococc
23	37	48.1	610	1 DNAK_BACSH	P069268 bacillus sp
24	37	48.1	610	1 DNAK_BACSL	P17820 bacillus su
25	37	48.1	613	1 DNAK_BACHD	Q9kd72 bacillus ha
26	37	48.1	613	1 DNAK_LACMK	087777 lactobacill
27	37	48.1	637	1 DNAK_PSEAE	Q9hv43 pseudomas
28	37	48.1	644	1 DNAK_LSCPN	Q32482 legionella
29	37	48.1	656	1 DNAK_COBNU	087712 coxiella bu
30	37	48.1	861	1 ORC1_HUMAN	013415 homo sapien
31	37	48.1	885	1 PMC2_HUMAN	Q01780 homo sapien
32	37	48.1	887	1 PKC2_MOUSE	P56960 mus musculus
33	37	48.1	1199	1 MFD_SYNPT3	Q55750 synechocystis

ALIGNMENTS

34	37	48.1	1377	1 NEOL_RAT	P97603 rattus norvegicus;
35	37	48.1	1461	1 NEO_HUMAN	Q92059 homo sapiens;
36	37	48.1	1477	1 HTK7_HYDAT	P25197 hydra attenuata
37	37	48.1	1493	1 NEOL_MOUSE	P97798 mus musculus
38	37	47.4	293	1 YC76_WYCTU	Q9p1x8 chlamydia trachomatis
39	36	46.8	158	1 YC76_WYCTU	Q11043 mycobacterium
40	36	46.8	269	1 NUDC_VIBCH	Q9kv27 vibrio cholerae
41	36	46.8	297	1 PECM_ERWCH	P42194 erwinia chrysanthemi
42	36	46.8	349	1 LDH_ALCEU	Q07251 alcaligenes eutrophus
43	36	46.8	388	1 AMPC_YEREN	P45460 yersinia enterocolitica
44	36	46.8	409	1 YOPM_YERPE	P17778 yersinia pestis
45	36	46.8	421	1 Y118_TREPA	Q83155 treponema pallidum

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TAXID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91347929; PubMed=1679007;
 RA Su M.-W., Suzuki H.R., Solursh M., Ramirez F.;
 RT "Progressively restricted expression of a new homeobox-containing
 gene during Xenopus laevis embryogenesis.";
 RT Development 111:1179-1187(1991).
 RL
 CC -!- SUBCELLULAR LOCATION: nuclear (Probable).
 CC -!- DEVELOPMENTAL STAGE: appears at the beginning of gastrulation.
 CC PLATEAU BETWEEN THE NEURULA AND MIDDLE-TAILBUD STAGES, AND
 CC DECREASE STEADILY THEREAFTER.
 CC -!- SIMILARITY: BELONGS TO THE MSH HOMEOBOX FAMILY.
 CC
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 or send an email to license@isb-sib.ch).
 DR EMBL: X50773; CAA41574.1; -.
 DR PIR: A60131; A60131.
 DR HSSP: P22808; 1NK3.
 DR InterPro: IPR001356; Homeobox.
 DR Pfam: PF00046; homeobox; 1.
 DR SMART: SM00389; HOXA_1.
 DR PROSITE: PS00227; HOMEBOX_1; 1.
 DR Homeobox; DNA-binding.
 KW NON_TER 1
 FT DNA_BIND 170 229 HOMEBOX.
 SQ SEQUENCE 295 AA; 32338 MW; 054331EBC106C10 CRC64;
 Query Match 51.9%; Score 40; DB 1; Length 295;
 Best Local Similarity 46.7%; Pred. No. 7.8;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 2 LPMSRPGVITASNLX 16
 DB 275 LPMSRPGVITASNLX 289
 RESULT 3
 Y312_METJIA STANDARD; PRT; 206 AA.
 ID Y312_METJIA
 AC Q57760; 01-NOV-1997 (Rel. 35, Created)
 AC 6-OCT-2001 (Rel. 40, Last annotation update)
 AC Hypothetical protein MJ0312.
 GN MJ0312.
 OS Methanococcus jannaschii.
 OC Archaea; Buryarchaeota; Methanococci; Methanococcales;
 Methanocaldococcaceae; Methanocaldococcus.
 NCBI_TAXID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RN STRAIN-JAI-1 / DSM 2661 / ATCC 43067;
 RN MEDLINE=95337939; PubMed=8688087;
 RA Built C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Gocayne J.D.,
 Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Shizuya H., Hunkapiller T.,
 Kerlavage A.R., Doucette-Brown L., Tomb J.F., Adams M.D., Reich C.I., Merrick J.M., Glodek A.,
 Overbeek R., Kirkness E.F., Weinstock G.M., Merrick J.M., Glodek A., Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Huston M.A., Rainey B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Weese C.R., Venter J.C.,
 RT Complete genome sequence of the methanogenic archaeon, Methanococcus

RT Jannaschii.";
 RRL Science 273:1058-1073(1996).
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL: U67486; AAB93309.1; -.
 DR PIR: MJ0312; -.
 DR HYPOTHETICAL PROTEIN; Complete Proteome.
 KW SEQUENCE 206 AA; 22367 MW; 1168AB576BF0E033A CRC64;
 SQ Query Match 50.6%; Score 39; DB 1; Length 206;
 Best Local Similarity 35.7%; Pred. No. 7.9;
 Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DLPMSPRGVITASNL 14
 DB 153 EFPISPEGGLIASI 166

RESULT 4
 STA3_HUMAN STANDARD; PRT; 770 AA.
 ID STA3_HUMAN
 AC P40765; 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Signal transducer and activator of transcription 3 (Acute-phase
 response factor).
 GN STAT3 OR APRF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Placenta:
 RX MEDLINE=94208062; PubMed=7512451;
 RA Akira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T.,
 RA Yoshida K., Sudo T., Naruto M., Kishimoto T.;
 RT "Molecular cloning of APRF, a novel IFN- γ -stimulated gene factor 3 (p91)
 related transcription factor involved in the gp130-mediated signalling
 pathway"; Cell 77:63-71(1994).
 RL [2]
 RP PHOSPHORYLATION ON SERINE.
 RX MEDLINE=95215845; PubMed=701321;
 RA Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S.;
 RT "Requirement of serine phosphorylation for formation of STAT-promoter
 complexes.;" Cell 26:1990-1994(1995).
 RL Science 267:1990-1994(1995).
 CC -!- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE INTERLEUKIN-6
 CC (IL-6) RESPONSIVE ELEMENTS IDENTIFIED IN THE PROMOTERS OF VARIOUS
 ACUTE-PHASE PROTEIN GENES.
 CC -!- PATHWAY: INVOLVED IN THE GP130-MEDIATED SIGNALING PATHWAY.
 CC -!- SUBUNIT: FORMS A HOMODIMER OR A HETERO-DIMER WITH A RELATED FAMILY
 CC MEMBER (AT LEAST STATE).
 CC -!- SUBCELLULAR LOCATION: Nuclear; translocated into the nucleus in
 CC response to phosphorylation.
 CC -!- TISSUE SPECIFICITY: Heart, Brain, Placenta, Lung, Liver, Skeletal
 CC MUSCLE, KIDNEY, AND PANCREAS.
 CC -!- PIM: TYROSINE PHOSPHORYLATION IN RESPONSE TO IL-6, IL-11, CNTF,
 CC IL-1, CSF-1, EGF, PDGF, TNF- α AND OSM. SERINE PHOSPHORYLATION
 CC IS IMPORTANT FOR THE FORMATION OF STABLE DNA-BINDING STAT3
 CC HOMODIMERS AND MAXIMAL TRANSCRIPTION ACTIVITY.
 CC -!- SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS.
 CC -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

EMBL: L29277; AAA58374.1; -.
 HSSP: P42227; 1BGL; -.
 TRANSFAC: T01493; -.
 Genew: HGNC:11364; STAT3.
 MMDB: 102582; -.
 InterPro: IPR000980; SH2.
 InterPro: IPR001217; STAT.
 Pfam: PF00017; SH2; 1.
 Pfam: PF01017; STAT; 1.
 Pfam: PF02864; STAT_bind; 1.
 Pfam: PF02865; STAT_prot; 1.
 SMART: SM00352; SH2; 1.
 PROSITE: PS00001; SH2; 1.
 Transcription regulation; DNA-binding; Nuclear protein;
 phosphorylation; SH2 domain.
 DOMAIN: 580 670 SH2.
 MOD_RES: 705 705 PHOSPHORYLATION (BY JAK) (BY SIMILARITY).
 NOD_RES: 727 727 PHOSPHORYLATION (BY SIMILARITY).
 SEQUENCE: 770 AA; 88052 MW; A3DCEB15B3B5360 CRC64;
 every Match 50.6%; Score 39; DB 1; Length 770;
 01-NOV-1995 (Rel. 32, Created)
 st Local Similarity 77.8%; Pred. No. 34;
 15-JUN-2002 (Rel. 41, Last annotation update)
 probable ribonuclease HI0526 precursor.
 HR0526
 HR0526
 Haemophilus influenzae.
 Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 Haemophilus.
 NCBI_TAXID=727;
 [1]
 SEQUENCE FROM N.A.
 RN26_HAEIN STANDARD; PRM; 272 AA.
 P44012; 01-NOV-1995 (Rel. 32, Created)
 01-NOV-1995 (Rel. 32, Last sequence update)
 15-JUN-2002 (Rel. 41, Last annotation update)
 probable ribonuclease HI0526 precursor.
 HR0526
 HR0526
 Haemophilus influenzae.
 Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 Haemophilus.
 NCBI_TAXID=727;
 [1]
 SEQUENCE FROM N.A.
 STRAINS-Rd / KW20 / ATCC 51907;
 MEDLINE=95550630; Published=1995-04-28;
 Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 McKenney K.R., Bult C.J., Tomb J.-F., Dougherty B.A., Marrick J.M.,
 McKenney K.R., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 Scott J.D., Shirley R., Liu L.I., Glodek A., Kelley J.M.,
 Weiland J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 Utterback T.R., Hanna M.C., Nguyen D.T., Sauder D.M., Brandon R.C.,
 Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
 Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 Venter J.C.;
 "Whole-genome random sequencing and assembly of *Haemophilus influenzae*
 Rd.";
 Science 269:496-512(1995).
 -- SIMILARITY: BELONGS TO THE RNASE T2 FAMILY.

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CC	entities requires a license agreement. (See http://www.isb-sib.ch/announce.html)
--	-- or send an email to license@isb-sib.ch).
DR	EMBL; U32735; AAC22192.1; .
DR	TIGR; H10526; .
DR	InterPro; IPR01168; RNase_T2.
DR	Pfam; PF00445; ribonuclease_1.
DR	PROSITE; PS00530; RNASE_T2.1; 1.
KW	DR PROSITE; PS00531; RNASE_T2.2; 1.
KW	HYPOTHETICAL PROTEIN; Hydrolase; Nuclease; Endonuclease; Signal;
KW	Complete proteome.
FT	SIGNAL 1 23 POTENTIAL, PROBABLE, RIBONUCLEASE HI0526.
FT	CHAIN 24 272 BY SIMILARITY.
FT	ACT_SITE 148 148 BY SIMILARITY.
FT	ACT_SITE 195 195 BY SIMILARITY.
FT	ACT_SITE 199 199 BY SIMILARITY.
SEQUENCE	272 AA; 31482 MW; 9d580ff9c2ceb392 CRC64;
Db	Query Match 49.4%; Score 38; DB 1; Length 272; Best Local Similarity 50.0%; Pred. No. 16; Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 170 DAPALPKKLLAQVL 183
RESULT 6	
ID_GPPA_CHLPN	STANDARD; PRT; 334 AA.
AC_Q9Z751;	16-OCT-2001 (rel. 40, Created)
DT_16-OCT-2001	(rel. 40, Last sequence update)
DT_15-JUN-2002	(rel. 41, Last annotation update)
DE_Glycerol-3-phosphate dehydrogenase (NAD(P)H-	Dependent glycerol-3-phosphate dehydrogenase (EC 1.1.1.94) (NAD(P)H-
GN_GSPA OR GPDA OR CPN0855 OR CP1014.	GSPA OR GPDA OR CPN0855 OR CP1014.
OS_Chlamydia pneumoniae (Chlamydophila pneumoniae).	Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC_Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.	Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX_NCBITaxon#83558;	NCBITaxon#83558;
RN_1]	[1]
RP_SEQUENCE FROM N.A.	
RC_STRAINS=CWL029;	
RX_MEDLINE=99206606; PubMed=10192388;	
RA_Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,	
RA_Olinger L., Grimm J., Davis R.W., Stepiens R.S.;	
RT_"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";	
RL_Nat. Genet. 21:385-389(1999).	
RN_[2]	[2]
RP_SEQUENCE FROM N.A.	
RC_STRAINS=AR39;	
RX_MEDLINE=20105255; PubMed=10684935;	
RA_Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,	
RA_Witte O., Hickley E.K., Peterson J., Utterback T., Berry K., Bass S.,	
RA_Hierl K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,	
RA_Gwynn M., Nelson W., Debey R., Kolonay J., McClarty G., Salzberg S.L.,	
RA_Eisen J., Fraser C.M., Fraser D., Smith K., Utterback T.,	
RT_Genome sequences of Chlamydia trachomatis MoPn and Chlamydia	
RT_pneumoniae AR39.";	
RL_Nucleic Acids Res. 28:1397-1406(2000).	
RN_3]	[3]
RP_SEQUENCE FROM N.A.	
RX_STRAINS=J138;	
RX_MEDLINE=2030349; PubMed=10871362;	
RA_Shiraishi M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,	
RA_Shiba T., Ishii K., Hattori M., Kuwara S., Nakazawa T.;	
RT_Comparison of whole genome sequences of Chlamydia pneumoniae J138	
RT_from Japan and CWL029 from USA.;"	
RL_Nucleic Acids Res. 28:2311-2316(2000).	
CC_-1-CATALYTIC ACTIVITY; SN-glycerol 3-phosphate + NAD(P)H) =	
CC_glycerone phosphate + NAD(P)H.	
-1 PATHWAY: De novo phospholipid biosynthesis; glycerol-3 phosphate	
CC - formation.	

CC -!- SUBCELLULAR LOCATION: cytoplasmic (Probable).
 CC -!- SIMILARITY: BELONGS TO THE NAD-DEPENDENT GLYCEROL-3-PHOSPHATE DEHYDROGENASE FAMILY.

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CC DR EMBL; AE01667; Aad18993.1; -;
 DR EMBL; AE002258; AAF3892.1; -;
 DR EMBL; AP002348; BRA99063.1; -;
 DR TIGR; CP1014; -;
 DR InterPro; IPR001652; NAD_GLY3P_dh;
 DR Pfam; PF01210; NAD_GLY3P_dh;
 DR PRINTS; PRO0077; GPDHRCNASE.
 DR PRODOM; PDD01649; NAD_GLY3P_dh; 1.
 DR PROSITE; PS00957; NAD_G3PDH; 1.
 DR PROSLIPID; NAD_Glyceraldehyde_3_phosphate_dehydrogenase; NAD: complete proteome. SEQUENCE 334 AA; 36161 MW; 4339ED6FFD7CEE6 CRC64;

Query Match 49.4%; Score 38; DB 1; Length 363;
 Best Local Similarity 40.0%; Pred. No. 22; Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0; Mismatches 0;

QY 2 LPMSPRGVITASNLXF 16
 Db 183 MPVKKGVVKSNYAF 197

RESULT 8 DR PIR; A45684; A45664. SQ SEQUENCE 363 AA; 43490 MW; DCBD20B50B078736 CRC64;

DNK STRAU ID DANK STRAU STANDARD; PRT; 590 AA.

AC 005942; DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DT Chaperone protein dnak (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70) (Fragment).

DE DE DNA.

GN OS Streptococcus mutans.

OC OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC NCBI_TAXID=1309;

RX RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GS-5; RX MEDLINE=97426041; PubMed=9282745;

RA Javaraman G.C.; Penders J.E.; Burne R.A.; RT "Transcriptional analysis of the Streptococcus mutans hrcA, grpe and dnak genes and regulation of expression in response to heat shock and environmental acidification."

RT RL Mol Microbiol; 25:329-341(1997).

CC -!- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
 CC -!- INDUCTION: BY HEAT SHOCK.
 CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

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CC DR EMBL; UT08296; AAC45612.1; -;
 DR HSSP; P0475; BPR.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS00136; HSP70_3; 1.
 KW Chaerone; ATP-binding; Heat shock; PHOSPHORYLATION (ATRO-); (BY SIMILARITY).

RT RC STRAIN=c6; RA Ayres M.D.; Howard S.C.; Kuzio J.; Lopez-Ferber M.; Possee R.D.; RT MEDLINE=94303173; PubMed=8030224; SEQUENCE FROM N.A.
 RT MEDLINE=94303173; PubMed=8030224; SEQUENCE FROM N.A.
 RT "The complete DNA sequence of *Autographa californica* nuclear polyhedrosis virus.";
 RT Virology 202:586-605(1994).

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CC DR EMBL; L07878; AAA16858.1; -;
 CC EMBL; L22658; AAA66669.1; -;

RESULT 9 DR PIR; A45684; A45664. SQ SEQUENCE 363 AA; 43490 MW; DCBD20B50B078736 CRC64;

ST3_MOUSE ID STA3_MOUSE STANDARD; PRT; 770 AA.

AC P42227; [1]

QY 1 DLPMSPRGVITASNLXF 16
 Db 432 DIPAPRGRVQIEVIE 447

Query Match 49.4%; Score 38; DB 1; Length 590;
 Best Local Similarity 43.8%; Pred. No. 38; Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0; Mismatches 0;

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE signal transducer and activator of transcription 3 (Acute-phase
 response factor).
 GN STAT3 OR APRF.
 OS MUS musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TAXID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 154-158; 181-185 AND 632-640.
 RC STRAIN=BALB/C; TISSUE=Liver;
 RX MEDLINE=4208062; PubMed=7515451;
 RA Akira S., Niitoh Y., Inoue M., Wang X.J., Shi W., Matsusaka T.,
 Yoshida K., Sudo T., Naruto M., Kishimoto T.; Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related transcription factor involved in the gp130-mediated signaling pathway.; J Biol Cell 77:63-71(1994).
 RL RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RX MEDLINE=94188718; PubMed=8140422;
 RA Hong Z., Wan Z., Darnell J.E. Jr.; STAT3: a STAT family member activated by tyrosine phosphorylation in response to epidermal growth factor and interleukin-6.; Science 264:95-98(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=5501485; PubMed=7523273;
 RA Raz R., Durbin J.E., Levy D.E.;
 RT "Acute phase response factor and additional members of the interferon-stimulated gene factor 3 family integrate diverse signals from cytokines, interferons, and growth factors.", J Biol. Chem. 269:24391-24395(1994).
 RN [4]
 RP SEQUENCE FROM N.A. (STAT3B).
 RC STRAIN=BALB/C, and C57BL/6; TISSUE=Liver;
 RX MEDLINE=9601616; PubMed=7568080;
 RA Scheffer T.S., Sanders L.K., Nathans D.; Cooperative transcriptional activity of Jun and Stat3 beta, a short form of Stat3.; Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101(1995).
 RN [5]
 RP PHOSPHORYLATION OF SER-727, AND MUTAGENESIS.
 MEDLINE=95354205; PubMed=754024;
 RA Wen Z., Zhong Z., Darnell J.E. Jr.;
 "Maximal activation of transcription by Stat1 and Stat3 requires both tyrosine and serine phosphorylation.", Cell 82:241-250(1995).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.
 RX MEDLINE=9833473; PubMed=9671298;
 RA Becker S., Groner B., Mueller C.W.;
 RT "Three-dimensional structure of the Stat3beta homodimer bound to DNA"; Nature 394:145-151(1998).
 CC -I- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE INTERLEUKIN-6 (IL-6)-RESPONSIVE ELEMENTS IDENTIFIED IN THE PROMOTERS OF VARIOUS ACUTE-PHASE PROTEIN GENES. STAT3B INTERACTS WITH THE N-TERMINAL PART OF C-JUN TO ACTIVATE SUCH PROMOTERS IN A COOPERATIVE WAY.
 CC -I- PATHWAY: INVOLVED IN THE GP130-MEDIATED SIGNALING PATHWAY.
 CC -I- SUBUNIT: FORMS A HOMODIMER OR A HETERO-DIMER WITH A RELATED FAMILY MEMBER (AT LEAST STAT1) (BY SIMILARITY).
 CC -I- SUBCELLULAR LOCATION: NUCLEAR; TRANSLOCATED INTO THE NUCLEUS IN response to phosphorylation.
 CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; STAT3A (SHOWN HERE) AND STAT3B; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -I- TISSUE SPECIFICITY: STAT3A IS SEEN IN THE LIVER, SPLEEN, AND KIDNEY. STAT3B IS ALSO DETECTED IN THE LIVER, ALTHOUGH IN A MUCH LESS ABUNDANT MANNER.

CC -I- PWM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-6, IL-11, CNTF, LIF, CSF-1, EGF, PDGF, IFN-ALPHA AND OSM. SERINE PHOSPHORYLATION IS IMPORTANT FOR THE FORMATION OF STABLE DNA-BINDING STAT3 HOMODIMERS AND MAXIMAL TRANSCRIPTIONAL ACTIVITY (BY SIMILARITY).
 CC -I- SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS.
 CC -I- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

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CC EMBL; L29278; AAC37254.1; -;
 CC DR EMBL; U06922; AAC19452.1; -;
 CC DR EMBL; U08378; AAC56668.1; -;
 CC DR EMBL; U30709; AAC52612.1; -;
 CC DR PDB; 1BG1; 13-JUN-99.
 CC DR TRANSC; T0154; -;
 CC DR MGD; MGI:03038; Stat3.
 CC DR InterPro; IPR00980; SH2.
 CC DR InterPro; IPR001217; STAT.
 CC DR Pfam; PF0017; SH2; 1.
 CC DR Pfam; PF0266; STAT_bind; 1.
 CC DR Pfam; PF02865; STAT_prot; 1.
 CC DR SMART; SM00252; SH2; 1.
 CC DR PROSITE; PS50001; SH2; 1.
 CC KW Transcription regulation; DNA-binding; Nuclear protein; SH2 domain; phosphorylation; Alternative splicing; 3D-structure.
 CC FT DOMAIN 580 670 SH2.
 CC FT MOD_RES 705 705 PHOSPHORYLATION (BY JAK) (BY SIMILARITY).
 CC FT VARSPLIC 727 727 TCNTNTDLPMSPTLDSLQEGNGEAEASAGQGEESLT FDDMLSECATSPM -> FIDAWK (IN ISOFORM STAT3B).
 CC FT VARIANT 701 701 MISSING (IN SOME CLONES).
 CC FT MUTAGEN 727 727 S->A; DECREASED TRANSCRIPTIONAL ACTIVATION.
 CC FT CONFLICT 16 25 E -> K (IN REF. 2); S -> T (IN REF. 2 AND 4).
 CC FT CONFLICT 394 394 M -> I (IN REF. 1).
 CC SQ SEQUENCE 770 AA; 88053 MW; 6C00626711C8012D CRC64;
 CC Query Match Best Local Similarity 49.4%; Score 38; DB 1; Length 770;
 CC Matches 7; Conservative 0; Pred. No. 51; Mismatches 0; Indels 0; Gaps 0;
 CC Qy 1 DLPMSPR 7
 CC Db 723 DLPMSPR 729

RESULT 10
 STA3_RAT STA3_RAT STANDARD; PRT; 770 AA.
 ID STA3_RAT
 AC P52631;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1995 (Rel. 34, Last sequence update)
 DR 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Signal transducer and activator of transcription 3.
 GN STAT3
 OS Rattus norvegicus (rat).
 OC Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; NCBI_TAXID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96102059; PubMed=8530402;
 RA Ripperger J.A., Fritz S., Richter K., Hocke G.M., Lottspeich F.,

Fey G.H.;
 RT "Transcription factors Stat3 and Stat5b are present in rat liver
 RT nuclei late in an acute phase response and bind interleukin-6
 RT response elements.";
 RL J. Biol. Chem. 270:29998-30006(1995).
 CC -!- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE INTERLEUKIN-6
 CC (IL-6)-RESPONSIVE ELEMENTS IDENTIFIED IN THE PROMOTERS OF VARIOUS
 CC ACUTE-PHASE PROTEIN GENES.
 CC -!- PATHWAY: INVOLVED IN THE GP130-MEDIATED SIGNALING PATHWAY.
 CC IS SUBUNIT: FORMS A HOMODIMER OR A HETERO-DIMER WITH A RELATED FAMILY
 CC MEMBER (AT LEAST SPAT1) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Nuclear; translocated into the nucleus in
 CC response to phosphorylation (BY SIMILARITY).
 CC -!- PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-6, IL-11, CNTF,
 CC LIF, CSP-1, EGF, PDGF, IFN-ALPHA AND OSM, SERINE PHOSPHORYLATION
 CC HOMODIMERS AND MAXIMAL TRANSCRIPTIONAL ACTIVITY (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS.
 CC -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

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DR EMBL; X91810; CAAE2920_1; -.
 DR HSSP; P42227; IBLG1.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF000017; SH2; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF02864; STAR_bind; 1.
 DR SMART; SM00252; SH2; 1.
 DR PROSITE; PS55001; SH2; 1.
 DR transcription regulation; DNA-binding; Nuclear protein;
 KW phosphorylation; SH2 domain.
 FT DOMAIN 580 SH2.
 FT MOD_RES 705 PHOSPHORYLATION (BY JAK) (BY SIMILARITY).
 FT SEQUENCE 727 729 MW; D74A0C76954754ED CRC64;

Query Match 49.4%; Score 38; DB 1; Length 770;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLPMSPR 7
 Db 723 DLPMSPR 729

RESULT 11

GYK	RAT	GAK_RAT	STANDARD;	PRT;	1305 AA.
		097874;			
		01-NOV-1997 (Rel. 35, Created)			
DT		16-OCT-2001 (Rel. 40, Last annotation update)			
DE		Cyclin G-associated kinase (EC 2.7.1.-), GAK.			
OS		Rattus norvegicus (Rat).			
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Rattus.			
OX		NCBI_TaxID=10116; [1]			
RN		SEQUENCE FROM N.A.			
RC		TISSUE=Kidney;			
RX		MEDLINE:97165969; PubMed=9013862;			
RA		Kanako Y., Kimura S.H., Okazaki I., Ikeda M., Nojima H.;			
		"GAK: a cyclin G associated kinase contains a tensin/auxilin-like			

RESULT 12

GYK	RAT	LRP1_CHICK	STANDARD;	PRT;	4543 AA.
		ID LRPI_CHICK			
		AC P98157;			
DT		01-OCT-1996 (Rel. 34, Created)			
DT		01-OCT-1996 (Rel. 34, Last sequence update)			
DT		16-OCT-2001 (Rel. 40, Last annotation update)			
DE		Low-density lipoprotein receptor-related protein 1 precursor (LRP1)			
DE		(Alpha-2-macroglobulin receptor) (A2MR).			
OS		Gallus gallus (Chicken).			
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OX		NCBI_TaxID=9031;			
RN		[1] SEQUENCE FROM N.A.			
RC		STRAIN=White leghorn; TISSUE=Liver, and Ovary;			
RX		MEDLINE:9410312; PubMed=7506255;			
RA		Nimpf J., Stifani S., Bilous P.T., Schneider W.J.;			

"the somatic cell-specific low density lipoprotein receptor-related protein of the chicken. Close kinship to mammalian low density lipoprotein receptor gene family members.";

J. BIOL. Chem. 269:211-219(1994).

-I- BIOLACTIN: INVOLVED IN THE PLASMA CLEARANCE OF CHYLOMICRON REMNANTS AND ACTIVATED ALPHA 2 MACROGLOBULIN, AS WELL AS THE LOCAL METABOLISM OF COMPLEXES BETWEEN PLASMINOGEN ACTIVATORS AND THEIR ENDODIGENOUS INHIBITORS. BINDS VITELLOGENIN, CALCIUM AND ALPHA 2-MACROGLOBULIN.

-I- ALTERNATIVE PRODUCTS: TYPE I membrane protein; 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.

-I- TISSUE SPECIFICITY: SOMATIC.

-I- PTM: CLEARED INTO A 85 kDa MEMBRANE-SPANNING SUBUNIT (LRP-85) AND A 515 kDa LANGE EXTRACELLULAR DOMAIN (LRP-515) THAT REMAINS NON-COVALENTLY ASSOCIATED.

-I- SIMILARITY: CONTAINS 22 EGF-LIKE DOMAINS.

-I- SIMILARITY: CONTAINS 31 LDL RECEPTOR CLASS A DOMAINS.

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CC FT DOMAIN 1181 1220 EGF-LIKE 5.
 RT FT DOMAIN 1221 1260 EGF-LIKE 6.
 RT FT DOMAIN 1534 1577 EGF-LIKE 7.
 RL FT DOMAIN 1842 1883 EGF-LIKE 8.
 CC FT DOMAIN 2151 2191 EGF-LIKE 9.
 CC FT DOMAIN 2472 2512 EGF-LIKE 10.
 CC FT DOMAIN 2516 2557 LDL-RECEPTOR CLASS A 11.
 CC FT DOMAIN 2558 2596 LDL-RECEPTOR CLASS A 12.
 CC FT DOMAIN 2597 2635 LDL-RECEPTOR CLASS A 13.
 CC FT DOMAIN 2636 2684 LDL-RECEPTOR CLASS A 14.
 CC FT DOMAIN 2688 2730 LDL-RECEPTOR CLASS A 15.
 CC FT DOMAIN 2730 2770 LDL-RECEPTOR CLASS A 16.
 CC FT DOMAIN 2770 2812 LDL-RECEPTOR CLASS A 17.
 CC FT DOMAIN 2814 2853 LDL-RECEPTOR CLASS A 18.
 CC FT DOMAIN 2854 2897 LDL-RECEPTOR CLASS A 19.
 CC FT DOMAIN 2900 2938 LDL-RECEPTOR CLASS A 20.
 CC FT DOMAIN 2939 2978 EGF-LIKE 11.
 CC FT DOMAIN 2979 3019 EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).

EMBL: X74904; CA52870.1; -.

CC FT DOMAIN 3287 3328 EGF-LIKE 13.
 CC FT DOMAIN 3329 3368 LDL-RECEPTOR CLASS A 21.
 CC FT DOMAIN 3369 3407 LDL-RECEPTOR CLASS A 22.
 CC FT DOMAIN 3408 3447 LDL-RECEPTOR CLASS A 23.
 CC FT DOMAIN 3448 3488 LDL-RECEPTOR CLASS A 24.
 CC FT DOMAIN 3489 3530 LDL-RECEPTOR CLASS A 25.
 PFAM: PR00008; EGF: 14.
 PFAM: PR0057; IgL_recept_A: 31.
 PFAM: PR0058; IgL_recept_B: 33.
 PRINTS: PRO0010; EGF_BLOOD.
 DR InterPro: IPR00561; EGF-like.
 DR InterPro: IPR00581; EGF_Ca.
 DR InterPro: IPR001438; EGF_II.
 DR InterPro: IPR002172; LDL_Recept_A.
 DR InterPro: IPR00033; LDL_Receptor_rep.
 SMART: SMM0001; EGF-like; 18.
 SMART: SMM0192; LDL_A; 31.
 SMART: SMM0135; LY; 34.
 PROSITE: PS00010; ASX_HYDROXYL; 3.
 PROSITE: PS00022; EGF_1; 5.
 PROSITE: PS01186; EGF_2; 7.
 PROSITE: PS01187; EGF_CA; 2.
 PROSITE: PS01209; LDL_A1; 27.
 PROSITE: PS0068; LDLR_2; 31.
 KW Receptor; Transmembrane; Repeat; Endocytosis; Glycoprotein;
 KW Signal; Calcium-binding; EGF-like domain; Coated pits;
 KW Alternative splicing.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 4543 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1.
 FT DOMAIN 22 4419 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 4420 4443 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 4444 4543 LDL-RECEPTOR CLASS A 1.
 FT DOMAIN 68 72 112 LDL-RECEPTOR CLASS A 2.
 FT DOMAIN 113 151 EGF-LIKE 1.
 FT DOMAIN 152 191 EGF-LIKE 2, CALCTUM-BINDING (POTENTIAL).
 FT DOMAIN 476 522 EGF-LIKE 3.
 FT DOMAIN 801 841 EGF-LIKE 4.
 FT DOMAIN 850 890 LDL-RECEPTOR CLASS A 3.
 FT DOMAIN 891 931 LDL-RECEPTOR CLASS A 4.
 FT DOMAIN 932 971 LDL-RECEPTOR CLASS A 5.
 FT DOMAIN 972 1011 LDL-RECEPTOR CLASS A 6.
 FT DOMAIN 1011 1058 1097 LDL-RECEPTOR CLASS A 7.
 FT DOMAIN 1100 1140 LDL-RECEPTOR CLASS A 8.
 FT DOMAIN 1141 1180 LDL-RECEPTOR CLASS A 9.
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 FT DOMAIN 2939 2978 EGF-LIKE 11.
 FT DOMAIN 2979 3019 EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).

DR HSSP: Q071954; IC18.
 DR InterPro: IPR00152; Asx_hydroxyl.
 DR InterPro: IPR00561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001438; EGF_II.
 DR InterPro: IPR002172; LDL_Recept_A.
 DR InterPro: IPR00033; LDL_Receptor_rep.
 SMART: SMM0001; EGF-like; 18.
 SMART: SMM0192; LDL_A; 31.
 PRINTS: PRO0010; EGF_BLOOD.
 SMART: SMM0179; EGF_Ca; 3.
 PROSITE: PS00010; ASX_HYDROXYL; 3.
 PROSITE: PS00022; EGF_1; 5.
 PROSITE: PS01186; EGF_2; 7.
 PROSITE: PS01187; EGF_CA; 2.
 PROSITE: PS01209; LDL_A1; 27.
 PROSITE: PS0068; LDLR_2; 31.
 DR SMART: SMM00135; LY; 34.
 PROSITE: PS00010; ASX_HYDROXYL; 3.
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 PROSITE: PS01186; EGF_2; 7.
 PROSITE: PS01187; EGF_CA; 2.
 PROSITE: PS01209; LDL_A1; 27.
 PROSITE: PS0068; LDLR_2; 31.
 DR SMART: SMM00135; LY; 34.
 PROSITE: PS00010; ASX_HYDROXYL; 3.
 PROSITE: PS00022; EGF_1; 5.
 PROSITE: PS01186; EGF_2; 7.
 PROSITE: PS01187; EGF_CA; 2.
 PROSITE: PS01209; LDL_A1; 27.
 PROSITE: PS0068; LDLR_2; 31.
 DR SMART: SMM0001; EGF-like; 18.
 SMART: SMM0192; LDL_A; 31.
 PRINTS: PRO0010; EGF_BLOOD.
 SMART: SMM0179; EGF_Ca; 3.
 PROSITE: PS00010; ASX_HYDROXYL; 3.
 PROSITE: PS00022; EGF_1; 5.
 PROSITE: PS01186; EGF_2; 7.
 PROSITE: PS01187; EGF_CA; 2.
 PROSITE: PS01209; LDL_A1; 27.
 PROSITE: PS0068; LDLR_2; 31.
 DR SMART: SMM00135; LY; 34.
 PROSITE: PS00010; ASX_HYDROXYL; 3.
 PROSITE: PS00022; EGF_1; 5.
 PROSITE: PS01186; EGF_2; 7.
 PROSITE: PS01187; EGF_CA; 2.
 PROSITE: PS01209; LDL_A1; 27.
 PROSITE: PS0068; LDLR_2; 31.
 DR SMART: SMM0001; EGF-like; 18.
 SMART: SMM0192; LDL_A; 31.
 PRINTS: PRO0010; EGF_BLOOD.
 SMART: SMM0179; EGF_Ca; 3.
 PROSITE: PS00010; ASX_HYDROXYL; 3.
 PROSITE: PS00022; EGF_1; 5.
 PROSITE: PS01186; EGF_2; 7.
 PROSITE: PS01187; EGF_CA; 2.
 PROSITE: PS01209; LDL_A1; 27.
 PROSITE: PS0068; LDLR_2; 31.
 DR SMART: SMM00135; LY; 34.
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 PROSITE: PS00022; EGF_1; 5.
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 SMART: SMM0179; EGF_Ca; 3.
 PROSITE: PS00010; ASX_HYDROXYL; 3.
 PROSITE: PS00022; EGF_1; 5.
 PROSITE: PS01186; EGF_2; 7.
 PROSITE: PS01187; EGF_CA; 2.
 PROSITE: PS01209; LDL_A1; 27.
 PROSITE: PS0068; LDLR_2; 31.
 DR SMART: SMM00135; LY; 34.
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 PROSITE: PS01186; EGF_2; 7.
 PROSITE: PS01187; EGF_CA; 2.
 PROSITE: PS01209; LDL_A1; 27.
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 DR SMART: SMM0001; EGF-like; 18.
 SMART: SMM0192; LDL_A; 31.
 PRINTS: PRO0010; EGF_BLOOD.
 SMART: SMM0179; EGF_Ca; 3.
 PROSITE: PS00010; ASX_HYDROXYL; 3.
 PROSITE: PS00022; EGF_1; 5.
 PROSITE: PS01186; EGF_2; 7.
 PROSITE: PS01187; EGF_CA; 2.
 PROSITE: PS01209; LDL_A1; 27.
 PROSITE: PS0068; LDLR_2; 31.
 DR SMART: SMM00135; LY; 34.
 PROSITE: PS00010; ASX_HYDROXYL; 3.
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 SMART: SMM0192; LDL_A; 31.
 PRINTS: PRO0010; EGF_BLOOD.
 SMART: SMM0179; EGF_Ca; 3.
 PROSITE: PS00010; ASX_HYDROXYL; 3.
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 DR SMART: SMM00135; LY; 34.
 PROSITE: PS00010; ASX_HYDROXYL; 3.
 PROSITE: PS00022; EGF_1; 5.
 PROSITE: PS01186; EGF_2; 7.
 PROSITE: PS01187; EGF_CA; 2.
 PROSITE: PS01209; LDL_A1; 27.
 PROSITE: PS0068; LDLR_2; 31.
 DR SMART: SMM0001; EGF-like; 18.
 SMART: SMM0192; LDL_A; 31.
 PRINTS: PRO0010; EGF_BLOOD.
 SMART: SMM0179; EGF_Ca; 3.
 PROSITE: PS00010; ASX_HYDROXYL; 3.
 PROSITE: PS00022; EGF_1; 5.
 PROSITE: PS01186; EGF_2; 7.
 PROSITE: PS011

FT	DISULFID	1020	1038	BY SIMILARITY.	RP	SEQUENCE FROM N.A.	
FT	DISULFID	1032	1049	BY SIMILARITY.	RX	MEDLINE=95203893; PubMed=534747;	
FT	DISULFID	1050	1073	BY SIMILARITY.	RA	Van Leuven F., Stas L., Hilliker C., Lorent K., Umans L., Serneels L., Overbergh L., Torrekens S., Moedhars D., De Srooper B., Van den Berghe H.,	
FT	DISULFID	1080	1086	BY SIMILARITY.	RT	"Structure of the gene (LRP1) coding for the human alpha 2-macroglobulin receptor lipoprotein receptor-related protein."	
FT	DISULFID	1102	1116	BY SIMILARITY.	RL	Genomics 24: 78-89 (1994).	
FT	DISULFID	1110	1129	BY SIMILARITY.	RN	[3]	
FT	DISULFID	1123	1138	BY SIMILARITY.	RP	SEQUENCE FROM N.A.	
FT	DISULFID	1143	1157	BY SIMILARITY.	RX	MEDLINE=93000812; PubMed=9782078;	
FT	DISULFID	1150	1170	BY SIMILARITY.	RA	Van Leuven F., Stas L., Thiry E., Nelissen B., Miyake Y., RNL	
FT	DISULFID	1164	1180	BY SIMILARITY.	RT	the lipoprotein receptor related protein: identification of one expressed mutation among 48 polymorphisms.",	
FT	DISULFID	1183	1194	BY SIMILARITY.	RN	[4]	
FT	DISULFID	1190	1204	BY SIMILARITY.	RP	PROCESSING.	
FT	DISULFID	1206	1219	BY SIMILARITY.	RX	MEDLINE=92069210; PubMed=2112085;	
FT	DISULFID	1225	1235	BY SIMILARITY.	RT	Herz J., Kowal R.C., Goldstein J.L., Brown M.S.,	
FT	DISULFID	1231	1244	BY SIMILARITY.	RA	"Proteolytic processing of the 600 kd low density lipoprotein receptor-related protein (LRP) occurs in a trans-Golgi compartment.",	
FT	DISULFID	1246	1259	BY SIMILARITY.	RT	EMBO J. 9:17669-1776(1990).	
FT	DISULFID	1358	1551	BY SIMILARITY.	RL	[5]	
FT	DISULFID	1547	1561	BY SIMILARITY.	RN	FUNCTION	
FT	DISULFID	1563	1576	BY SIMILARITY.	RP	MEDLINE=91092405; PubMed=1702392;	
FT	DISULFID	1846	1857	BY SIMILARITY.	RA	Kristensen T., Moestrup S.K., Glemann J., Bendtsen L., Sand O.,	
FT	DISULFID	1869	1882	BY SIMILARITY.	RT	Sottrup-Jensen L.,	
FT	DISULFID	2155	2166	BY SIMILARITY.	RT	"Evidence that the newly cloned low-density lipoprotein receptor-related protein (LRP) is the alpha 2-macroglobulin receptor.",	
FT	DISULFID	2176	2176	BY SIMILARITY.	RL	FEBs Lett. 276:151-155(1990).	
FT	DISULFID	2476	2487	BY SIMILARITY.	RN	[6]	
FT	DISULFID	2483	2497	BY SIMILARITY.	RP	STRUCTURE BY NMR OF 105-1100.	
FT	DISULFID	2499	2511	BY SIMILARITY.	RX	MEDLINE=925972; PubMed=10318830;	
FT	DISULFID	2518	2531	BY SIMILARITY.	RA	Huang W., Dolmer K., Geitins P.G.W.,	
FT	DISULFID	2526	2544	BY SIMILARITY.	RT	"NMR solution structure of complement-like repeat CR8 from the low density lipoprotein receptor-related protein.",	
FT	DISULFID	2538	2555	BY SIMILARITY.	RL	J. Biol. Chem. 274:14110-14136(1999).	
FT	DISULFID	2560	2572	BY SIMILARITY.	CC	AND ACTIVATED ALPHA 2 MACROGLOBULIN, AS WELL AS THE LOCAL METABOLISM OF COMPLEXES BETWEEN PLASMINOGEN ACTIVATORS AND THEIR ENDGENOUS INHIBITORS.	
FT	DISULFID	2567	2585	BY SIMILARITY.	CC	- - SUBCELLULAR LOCATION: Type I membrane protein.	
FT	DISULFID	2579	2594	BY SIMILARITY.	CC	- - TISSUE SPECIFICITY: MOST ABUNDANT IN LIVER, BRAIN AND LUNG.	
FT	DISULFID	2611	2624	BY SIMILARITY.	CC	- - PTM: CLEAVED INTO A 85 kDa MEMBRANE SPANNING SUBUNIT (LRP-85) AND A 515 kDa LARGE EXTRACELLULAR DOMAIN (LRP-515) THAT REMAINS NON-COVALENTLY ASSOCIATED.	
Db	2453	DIPQQPMGIIA	2463	Indels	0;	CC	- - SIMILARITY: CONTAINS 22 ESP-LIKE DOMAINS.
RESULT 13				Caps	0;	CC	- - SIMILARITY: CONTAINS 31 LDL-RECEPTOR CLASS A DOMAINS.
QY	1	DLPLMSPRGVIA	11	Score 38; DB 1;	Length 4543;	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is modified and this statement is not removed. Usage by commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
ID	LRPL_HUMAN	STANDARD;	PRT;	4544 AA.		CC	-----
AC	007954;	:				CC	-----
DT	01-OCT-1996	(Rel. 34, Created)				CC	-----
DT	01-OCT-1996	(Rel. 34, Last sequence update)				CC	-----
DE	Low-density lipoprotein receptor-related protein 1 precursor (LRP) (Alpha-2-macroglobulin receptor) (A2MR) (Apolipoprotein E receptor LRP1 OR A2MR).					CC	-----
OC	Homo sapiens (Human).					CC	-----
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					CC	-----
NCBI_TAXID	9606;					CC	-----
[1]	SEQUENCE FROM N.A.					CC	-----
RC	TISSUE=Liver;					CC	-----
RX	MEDLINE=8210795; PubMed=3266596;					DR	DR
RA	Herz J., Hamann U., Rogne S., Myklebost O., Gausepohl H., Stanley K.K.;					DR	MIM: 107770; -
RT	"Surface location and high affinity for calcium of a 500-kd liver membrane protein closely related to the LDL-receptor suggest a physiological role as lipoprotein receptor.";					DR	InterPro; IPR00152; Asx_Hydroxyl.
RT	physiological role as lipoprotein receptor.";					DR	InterPro; IPR000561; EGF-like.
RL	EMBO J. 7:4119-4127(1988).					DR	InterPro; IPR001881; EGF_a.
RN	[2]					DR	InterPro; IPR002172; LDL_recept_A.
RP						DR	InterPro; IPR00033; LDL_receptor_rep.
RC						DR	InterPro; IPR00057; ldl_recept_a; 31.
						DR	Pfam; PF00058; ldl_recept_b; 33.
						DR	PRINTS; PR00261; LDLRECEPTOR.

SMART; SMO001: EGF_CA; 3.	FT	SITE	4502	4507	ENDOCYTOSIS SIGNAL (POTENTIAL).
SMART; SMO012; LDLa; 31.	FT	DISULFID	27	40	BY SIMILARITY.
SMART; SMO0135; LY; 32.	FT	DISULFID	34	53	BY SIMILARITY.
PROSTE; PS00010; ASX_HYDROXYL; 3.	FT	DISULFID	47	64	BY SIMILARITY.
PROSTE; PS00022; EGF_1; 5.	FT	DISULFID	72	85	BY SIMILARITY.
PROSTE; PS0116; EGF_2; 8.	FT	DISULFID	79	98	BY SIMILARITY.
PROSTE; PS0117; EGF_CA; 2.	FT	DISULFID	92	108	BY SIMILARITY.
PROSTE; PS01209; LDRA_1; 27.	FT	DISULFID	115	124	BY SIMILARITY.
DR	FT	DISULFID	120	133	BY SIMILARITY.
DR	FT	DISULFID	135	148	BY SIMILARITY.
KW	FT	DISULFID	154	164	BY SIMILARITY.
KW	FT	DISULFID	160	173	BY SIMILARITY.
SIGNAL; Calcium-binding; EGF-LIKE domain; Coated Pits; 3D-structure.	FT	DISULFID	175	188	BY SIMILARITY.
CHAIN	20	4544	POTENTIAL.		
DOMAIN TRANSMEM	20	4419	LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1.		
DOMAIN	4420	4444	EXTRACELLULAR (POTENTIAL).		
DOMAIN	4445	4544	POTENTIAL.		
DOMAIN	25	66	CYTOSPLASMIC (POTENTIAL).		
DOMAIN	70	110	LDL-RECEPTOR CLASS A 1.		
DOMAIN	111	149	LDL-RECEPTOR CLASS A 2.		
DOMAIN	150	189	EGF-LIKE 1.		
DOMAIN	474	520	EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).		
DOMAIN	803	843	EGF-LIKE 3.		
DOMAIN	852	892	EGF-LIKE 4.		
DOMAIN	893	933	LDL-RECEPTOR CLASS A 3.		
DOMAIN	934	973	LDL-RECEPTOR CLASS A 4.		
DOMAIN	1013	1053	LDL-RECEPTOR CLASS A 5.		
DOMAIN	1060	1099	LDL-RECEPTOR CLASS A 6.		
DOMAIN	1142	1182	LDL-RECEPTOR CLASS A 7.		
DOMAIN	1183	1222	LDL-RECEPTOR CLASS A 8.		
DOMAIN	1262	1326	LDL-RECEPTOR CLASS A 9.		
DOMAIN	1536	1579	LDL-RECEPTOR CLASS A 10.		
DOMAIN	1846	1887	EGF-LIKE 5.		
DOMAIN	2155	2195	EGF-LIKE 6.		
DOMAIN	2478	2518	EGF-LIKE 7.		
DOMAIN	2522	2563	EGF-LIKE 8.		
DOMAIN	2564	2602	EGF-LIKE 9.		
DOMAIN	2603	2641	EGF-LIKE 10.		
DOMAIN	2642	2690	LDL-RECEPTOR CLASS A 11.		
DOMAIN	2694	2732	LDL-RECEPTOR CLASS A 12.		
DOMAIN	2732	2771	LDL-RECEPTOR CLASS A 13.		
DOMAIN	2772	2814	LDL-RECEPTOR CLASS A 14.		
DOMAIN	2816	2855	LDL-RECEPTOR CLASS A 15.		
DOMAIN	2856	2899	LDL-RECEPTOR CLASS A 16.		
DOMAIN	2902	2940	LDL-RECEPTOR CLASS A 17.		
DOMAIN	2941	2981	LDL-RECEPTOR CLASS A 18.		
DOMAIN	2982	3022	LDL-RECEPTOR CLASS A 19.		
DOMAIN	3290	3371	LDL-RECEPTOR CLASS A 20.		
DOMAIN	3372	3410	EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).		
DOMAIN	3411	3450	EGF-LIKE 13.		
DOMAIN	3491	3491	EGF-LIKE 14.		
FT	3492	3533	EGF-LIKE 15.		
FT	3574	3572	EGF-LIKE 16.		
FT	3573	3611	EGF-LIKE 17.		
FT	3611	3649	EGF-LIKE 18.		
FT	3652	3692	EGF-LIKE 19.		
FT	3693	3733	EGF-LIKE 20.		
FT	3739	3778	EGF-LIKE 21.		
FT	3823	3823	EGF-LIKE 22.		
FT	3824	3861	RECOGNITION SITE FOR PROTEOLYTICAL PROCESSING (POTENTIAL).		
FT	4147	4183	RECOGNITION SITE FOR PROTEOLYTICAL PROCESSING (POTENTIAL).		
FT	4196	4232	RECOGNITION SITE FOR PROTEOLYTICAL PROCESSING (POTENTIAL).		
FT	4232	4268	RECOGNITION SITE FOR PROTEOLYTICAL PROCESSING (POTENTIAL).		
FT	4268	4304	RECOGNITION SITE FOR PROTEOLYTICAL PROCESSING (POTENTIAL).		
FT	4304	4340	RECOGNITION SITE FOR PROTEOLYTICAL PROCESSING (POTENTIAL).		
FT	4375	4409	RECOGNITION SITE FOR PROTEOLYTICAL PROCESSING (POTENTIAL).		
FT	3940	3943	RECOGNITION SITE FOR PROTEOLYTICAL PROCESSING (POTENTIAL).		
RC			Query Match		
RC			Best local Similarity	49.4%	Score 38; DB 1; Length 4544;
RC			Matches	54.5%	Pred. No. 3 6e+02;
RC				2;	Mismatches 3;
RC					Indels 0;
RC					Gaps 0
Qy	1	DIPMSPRGVIA	11		
Db	2459	DIPQPPMGITA	2469		
RESULT 14					
FLC_ARATH					
ID					
FLC_ARATH					
STANDARD;					
PRM;					
196 AA.					
AC	Q957Q7;				
DT	15-JUN-2002 (Rel. 41, Created)				
DT	15-JUN-2002 (Rel. 41, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	FLOWERING LOCUS C protein (MADS box protein)				
GN	FLC OR FLP OR AT5G1040 OR T31P16_130.				
OS	Arabidopsis thaliana (Mouse-ear cress).				
OC	Eukaryota; Viridiplantae; Streptophytina; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;				
OC	eurosid I; II; Brassicales; Brassicaceae; Arabidopsis.				
OX	NCBL_TAXID=3702; Brassicaceae;				
RN	[1]				
RC	SEQUENCE FROM N.A.				
RC	STRAIN=Cv, C24, and cv. Columbia;				
RC	MEDLINE-99172058; PubMed=10072403;				
RA	Sheldon C.C., Burn J.E., Perez P.F., Metzger J., Edwards J.A.,				
RA	Peacock W.J., Dennis E.S.,				
RT	"The FLP MADS box gene: A repressor of flowering in Arabidopsis				
RT	regulated by vernalization and methylation";				
RL	Plant Cell 11:445-458(1999).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-99264314; PubMed=10330478;				
RA	Michaels S.D., Amasino R.M.;				
RA	"FLOWERING LOCUS C encodes a novel MADS domain protein that acts as a				
RT	repressor of flowering";				
RL	Plant Cell 11:949-956(1999).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Cv, Columbia;				

RX MEDLINE=21016721; PubMed=11130714;
 RA Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asamizu E.,
 RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashita K.,
 RA Nakazaki N., Naruo K., Okumura S., Shioji S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,
 RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
 RA Habermann K., Murray J., Johnson D., Rohlfing T., Nelson J.,
 RA Stoenking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M.,
 RA Belter E., Cordium M., Courtnay L., Courtney W., Danie M.,
 RA Du H., Edwards J., Fryman J., Hackney E., Lamar E., Latrelle P.,
 RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strohmatt C.,
 RA Wagner McPherson C., Wollan A., Yoakim M., Bell M., Dedhia N.,
 RA Parnell L., Shah R., Rodriguez M., Hojn See L., Vil D., Baker J.,
 RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
 RA Martienssen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,
 RA Volkert G., Wambutt R., Duesterhoft A., Stilekema W., Pohl T.,
 RA Entian K.-D., Terkyn N., Hartley N., Bent E., Johnson S.,
 RA Langham S.A., McCullagh B., Robben B., Grymonpre B., Zimmermann W.,
 RA Ramsperger U., Wedler H., Balke K., Wedler E., Peters S.,
 RA van Straveren M., Dirise W., Moolijman P., Klein Lankhorst R.,
 RA Weitzenegger T., Bothe G., Rose M., Hauf J., Bernreiser S., Hempel S.,
 RA Feldpausch M., Lamberth S., Villarreal R., Gielen J., Ardiles W.,
 RA Bents O., Lemcke K., Kolesov G., Mayer K.F.X., Rudd S., Schoof H.,
 RA Schueler C., Zaccaria P., Meves H.-W., Bevan M., Fraenz P.,
 RA thalidomide"; "Sequence and analysis of chromosome 5 of the plant *Arabidopsis*
Nature 408:823-826(2000).
 [4]
 RP FUNCTION.
 RC STRAIN>V. PI-0;
 RX MEDLINE=20202708; PubMed=10716723;
 RA Sheldon C.C., Rouse D.T., Finnegan E.J., Peacock W.J., Dennis E.S.;
 RT LOCUS C (FLC)."; "The molecular basis of vernalization: the central role of FLOWERING
 PROC. NATL. ACAD. SCI. U.S.A. 97:3753-3758(2000).
 [5]
 RP FUNCTION.
 RC STRAIN>CV. Columbia;
 RX MEDLINE=21178818; PubMed=11283346;
 RA Michaels S.D., Amasino R.M.;
 "Loss of flowering locus c activity eliminates the late-flowering
 phenotype of frigida and autonomous pathway mutations but not
 responsiveness to vernalization.";
 RL Plant Cell 13:935-942(2001).
 CC -!- FUNCTION: Putative transcription factor that seems to play a
 central role in the regulation of flowering time in the late-
 and the vernalization flowering pathways. Inhibits flowering by
 repressing 'SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1'.
 CC -!- TISSUE SPECIFICITY: Nuclear (Probable).
 CC -!- TISSUE AND LOWER EXPRESSION IN THE VEGETATIVE APEX AND IN
 IN YOUNG TISSUES OF THE INFLORESCENCE.
 CC -!- DEVELOPMENTAL STAGE: FOUND IN SHOOTS OF NON-FLOWERING PLANTS GROWN
 UNDER LONG-DAY CONDITIONS AT DAYS 4 TO 15, AND IN SHOOTS OF PLANTS
 GROWN UNDER SHORT-DAY CONDITIONS AT DAYS 4 TO 11 AFTER
 GERMINATION.
 CC -!- INDUCTION: EPITHELIOGENETICALLY DOWNREGULATED BY VERNALIZATION.
 CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 FACTORS.
 CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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 or send an email to license@isb-sib.ch).
 DR EMBL; AF116528; ADD21249.1; -.
 DR EMBL; AF116527; ADD21248.1; -.
 DR EMBL; AF116528; ADD21249.1; -.
 DR EMBL; AF116527; ADD21248.1; -.
 DR EMBL; PS00107; PROTEIN_KINASE_ATP; PARTIAL.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; PARTIAL.
 DR PROSITE; PS00101; PROTEIN_KINASE_DOM; PARTIAL.
 DR PROSITE; PS00636; DNAJ_1; FALSE_NEG.

DR EMBL; AL355332; CAB92055.1; -.
 DR HESPB; P11746; IMM.
 DR TRANSFAC; T03284; -.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF00319; SRF-TP; 1.
 DR Pfam; PF01486; K-box; 1.
 DR PRINTS; PR00404; MADS_DOMAIN.
 DR SMAP; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; FALSE_NEG.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 KW Transcription regulation; Repressor; DNA-binding; Flowering;
 KW Developmental protein; Nuclear protein.
 FT DOMAIN 3 57 MADS,
 DOMAIN 68 166 K-30X.
 FT SEQUENCE 196 AA; 21865 MW; 656085A2B157FF42 CRC64;
 OY 1 DLPMSPRGVIASNL 14
 Query Match 48.1%; Score 37; DB 1; Length 196;
 Best Local Similarity 50.0%; Pred. No. 17; Mismatches 7; Conservative 3; Indels 4; Gaps 0; Gaps 0;
 Db 175 EMEMSPAGQISDNL 188
 DB Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

RESULT 15
 GAK_MOUSE
 ID GAK_MOUSE STANDARD; PRT; 499 AA.
 AC Q9KX4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Cyclin G-associated kinase (EC 2.7.1.-) (Fragment).
 GN GAK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1] NEBL_TAXID=10090;
 RP SEQUENCE FROM N.A.
 RC TISSUE>Breast tumor;
 RA Strausberg R.;
 RL Submitted (FEB 2001) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Associates with cyclin G and CDK5. Seems to act as an
 auxillin homolog that is involved in the uncoupling of clathrin-
 coated vesicles by Hsc70 in non-neuronal cells. Expression
 oscillates slightly during the cell cycle, peaking at G1 (By
 similarity).
 CC -!- SUBCELLULAR LOCATION: Localizes to the perinuclear area and to the
 trans-Golgi network. Also seen on the plasma membrane, probably at
 foci of adhesions (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -!- SIMILARITY: CONTAINS 1 J DOMAIN.
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 or send an email to license@isb-sib.ch).
 DR EMBL; BC003958; AAH03958 1; -.
 DR InterPro; IPR001623; DNAJ_N.
 DR InterPro; IPR000719; Euk_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00226; DNAJ; 1.
 DR SMART; SM00271; DNAJ; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; PARTIAL.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; PARTIAL.
 DR PROSITE; PS00101; PROTEIN_KINASE_DOM; PARTIAL.
 DR PROSITE; PS00636; DNAJ_1; FALSE_NEG.

CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

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DR EMBL; AB017035; BAB03215.1; -

DR HSSP; P04475; IDG4.

DR InterPro; IPR001023; Hsp70.

DR pfam; PF00012; Hsp70.1.

DR PRINTS; PR00301; HEATSHOCK70.

DR ProdDom; P000089; Hsp70.1.

DR PROSITE; PS00297; HSP70_1; 1.

DR PROSITE; PS0029; HSP70_2; 1.

KW Chaperone; ATP-binding; Heat shock; Phosphorylation.

FT INIT-MET 0 BY SIMILARITY.

FT MOD-RES 168 168 BY SIMILARITY.

SO SEQUENCE 606 AA; 65951 MW; 7955FD3JDB845F56 CRC64;

OY 1 DLPMSPRGVIASNLXF 16 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

Db 426 DIPAPARPGVPQIEVTF 441

Best local similarity 48.1%; Score 37; DB 1; Length 606;

Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

DT 01-NOV-1995 (Rel. 32, Created)

DE Chaperone protein dnak (heat shock protein update)

DE protein) (HSP70).

GN DNAK OR IL0954.

OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis), and

OC bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.

OX NCBI_TAXID=1360, 1359;

RN [1]

AC P42368; Q0CGY8;

RP SEQUENCE FROM N.A.

RC SPECIES="L.l.cremoris"; STRAIN=MG1363;

RC MEDLINE=94172317; PubMed=8126443;

RA Raton Y.J., Shearman C.A., Gasson M.J.,

RT "Cloning and sequence analysis of the dnak gene region of Lactococcus

J. Gen. Microbiol. 139:3263-3263(1993).

[2]

SEQUENCE FROM N.A.

RC SPECIES="L.l.lactis"; STRAIN=LM0230;

RC MEDLINE=9237496; PubMed=8181763;

RA Barilli M.J.S., Kim S.G., Batt C.A.;

RT "Cloning and sequencing of the Lactococcus lactis subsp. lactis dnak

RT gene using a PCR-based approach.";

RL Gene 142:91-96(1994).

RN [3]

RP SEQUENCE FROM N.A.

RC SPECIES="L.l.lactis"; STRAIN=IL1403;

RC MEDLINE=21235186; PubMed=1133471;

RA Boilotin A., Wincker P., Mauder S., Jaillon O., Malarme K.,

RA Weissenbach J., Enlich S.D., Sorokin A.;

RT "The complete genome sequence of the lactic acid bacterium Lactococcus

RT lactis ssp. lactis IL1403.";

RL Genome Res. 11:731-753(2001).

CC -!- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).

CC -!- INDUCTION: BY STRESS CONDITIONS E.G. HEAT SHOCK BY SIMILARITY.

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DR EMBL; X76642; CAAS54089.1; -

DR DR EMBL; AE005329; AAK0505.2.1; -

DR HSSP; P04475; IDG4.

DR InterPro; IPR001023; Hsp70.

DR pfam; PF00012; HSP70_1.

DR PRINTS; PR00301; HEATSHOCK70.

DR ProdDom; PD000089; Hsp70.1.

DR PROSITE; PS00297; HSP70_2; 1.

DR PROSITE; PS0029; HSP70_3; 1.

KW Chaperone; ATP-binding; Heat shock; Phosphorylation.

FT INIT-MET 0 BY SIMILARITY.

FT MOD-RES 168 168 BY SIMILARITY.

SO SEQUENCE 607 AA; 64948 MW; 567FA7160313310E CRC64;

OY 1 DLPMSPRGVIASNLXF 16 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

Db 431 DIPAPARPGVPQIEVTF 446

Best local similarity 48.1%; Score 37; DB 1; Length 607;

Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Chaperone protein dnak (heat shock protein update)

DE protein) (HSP70).

GN DNAK OR SP0517.

OS Streptococcus pneumoniae.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TAXID=1313;

RN [1]

RP SEQUENCE FROM N.A.

RC RT Rioux C.R., Marin D., Hanel J., Brodeur B.R.;

RT RT "Heat shock protein HSP70 and amino terminus of Dnaj of Streptococcus

RT pneumoniae.";

RT Submitted (Sep-1996) to the EMBL/GenBank/DDJB databases.

RN [2]

RP SEQUENCE FROM N.A.

RC RT Rioux C.R., Marin D., Hanel J., Brodeur B.R.;

RT RT "Heat shock protein HSP70 and amino terminus of Dnaj of Streptococcus

RT pneumoniae.";

RT Submitted (Sep-1996) to the EMBL/GenBank/DDJB databases.

RN [3]

RP SEQUENCE FROM N.A.

RC RT Rioux C.R., Marin D., Hanel J., Brodeur B.R.;

RT RT "Heat shock protein HSP70 and amino terminus of Dnaj of Streptococcus

RT pneumoniae.";

RT Submitted (Sep-1996) to the EMBL/GenBank/DDJB databases.

RN [4]

RP SEQUENCE FROM N.A.

RC RT Kim S.-W., Choi I.-H., Kim S.-N., Pyo S.-N., Rhee D.-K.;

RT RT "Molecular cloning, expression, and characterization of dnak in

RT Streptococcus pneumoniae.";

RT FEMS Microbiol. Lett. 161:217-224(1998).

RC RP STRAIN=TIGR4;

RX MBDLMB-21357209; PubMed=11463916;
 RA Tettelein H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
 Peterson S., Heidelberg J., Deboy R.T., Haft D.H., Dodson R.J.,
 Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
 Holtapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
 RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
 RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Ventter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.,
 RT "Complete genome sequence of a virulent isolate of Streptococcus
 pneumoniae";
 RL Science 293:498-506 (2001).

CC CCGC - FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
 CC CCGC - INDUCTION: BY STRESS CONDITIONS E.G. HEAT SHOCK (BY SIMILARITY).

CC CCGC - SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

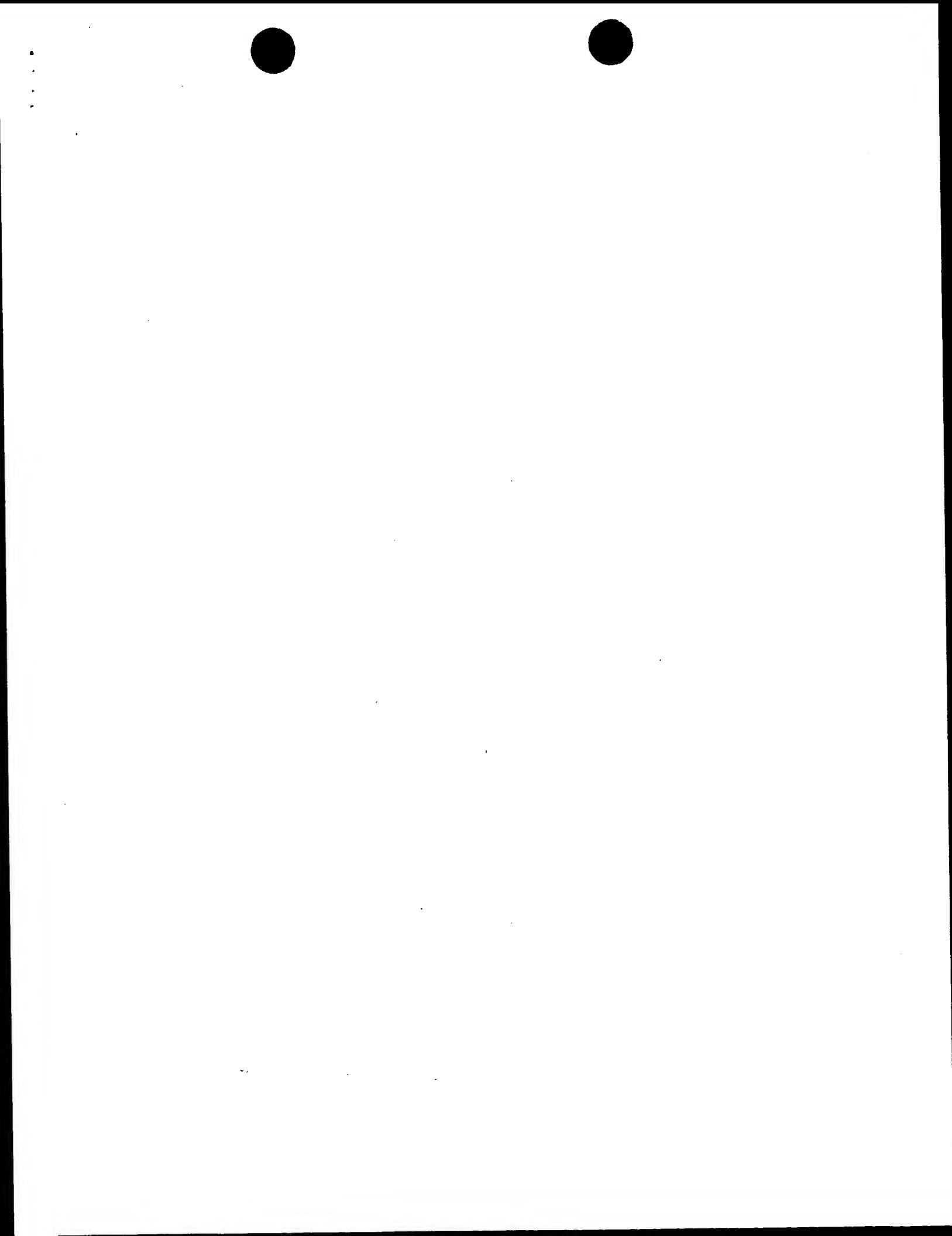
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DR EMBL; U73720; AAB39211.; .
 DR EMBL; U84387; AAC18921.; .
 DR EMBL; AED007363; AAK74675.; .
 DR HSSP; P04475; 1DG4.
 DR TIGR; SP0517.; .
 DR InterPro; IPR001023; HSP70.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS00329; HSP70_3; 1.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PRO0301; HEATSHOCK70.
 DR PRODOM; PD000089; HSP70; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS00329; HSP70_3; 1.
 KW Chaperone; ATP-binding; Heat shock; Phosphorylation;
 KW Complete proteome.
 FT MOD_RES 173 173 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CONFLICT 493 493 A -> P (IN REF. 2).
 FT CONFLICT 495 495 A -> S (IN REF. 1).
 FT CONFLICT 530 530 A -> P (IN REF. 2).
 FT CONFLICT 556 556 T -> A (IN REF. 1 AND 2).
 FT CONFLICT 601 602 DG -> E (IN REF. 2).
 SQ SEQUENCE 607 AA: 64842 MW: 11D626F1B37D0760 CRC64;

Query Match 48.1%; Score 37; DB 1; Length 607;
 best local similarity 37.5%; Pred. No. 60;
 matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DLPMSPRGVIASNLXF 16
 Db 431 DIPMAPRGIPQIEWTF 446

Search completed: January 2, 2003, 12:03:45
 Job time : 35 secs



	DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE	4921517D2IRIK	protein.
GN	4921517D2IRIK	
OS	Mus musculus (Mouse)	
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N A.	
RC	STRAIN=C57BL/6J;	TISSUE=TESTIS;
RX	MEDLINE=21085660;	PubMed=1121851;
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Akarawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Kaito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J., Schriml L.M., Staubli F., Suzuki K., Tomita M., Wagner L., Sakai K., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustinich S., Hill D., Hofmann M., Hume D.A., Kameya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzairelli J., Monbaerts P., Nordone P., Ring B., Rinwold M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shiba Y., Whitaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;	
RA	Nature 409:685-690(2001);	
RA	EMLB: AK01926; BAB9623_1; -	
RL	Nature 409:685-690(2001);	
DR	EMBL: MG1:1914972; 4921517D2IRIK.	
DR	InterPro: IPR004000; Actin_like.	
DR	pfam: PF00022; actin_1.	
DR	SMART: SM00268; actin_1.	
DR	SMART: SW00268; ACTIN_1.	
SQ	SEQUENCE 1207 AA; 130803 MW; 2CA2CD754C0F5DB CRC64;	
DB	400 LPMSPRGVIAS 410	
RA	Query Match 57.1%; Score 44; DB 11; Length 1096; Best Local Similarity 81.8%; Pred. No. 35; DR 9; Conservative Matches 9; Mismatches 0; Indels 2; Gaps 0; Gaps 0;	
RA	RT "Functional annotation of a full-length mouse cDNA collection.";	
RA	RT Nature 409:685-690(2001);	
RA	RT EMBL: MG1:1914972; 4921517D2IRIK.	
RA	RT InterPro: IPR004000; Actin_like.	
RA	RT pfam: PF00022; actin_1.	
RA	RT SMART: SM00268; actin_1.	
RA	RT SMART: SW00268; ACTIN_1.	
RA	RA 1096 AA; 110401 MW; EB5E1FS1D0A1C983 CRC64;	
RA	RA 08U8M0	
RA	RA 08U8M0	
AC	08U8M0;	PRELIMINARY;
AC	08U8M0;	PRT; 184 AA.
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)	
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
DE	Sarcosine oxidase gamma subunit.	
GN	SOXG OR ATU4070 OR ASR.L.1572.	
OS	Agrobacterium tumefaciens (strain C58 / ATCC 33970)	
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;	
OC	Rhizobiaceae; Rhizobium.	
OX	NCBI_TaxID=176299;	
RN	[1]	
RP	SEQUENCE FROM N A.	
RA	MEDLINE=2150850;	PubMed=11743193;
RA	Wood D.W., Settahal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovے D. Sr., Chapman P., Clelandening J.J., Deatheeage G., Gillet W., Grant C., Ruytavijn T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saemphimachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Kreepan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Lester E.W., -	
RA	RT "The genome of the natural genetic engineer Agrobacterium tumefaciens C58.";	
RA	RT Science 294:2317-2323(2001).	
RA	RA [2]	
RP	SEQUENCE FROM N A.	
RX	MEDLINE=2160851;	PubMed=1743194;
RA	Goodier B., Hinkle G., Gattou M., Miller N., Blanchard M., Mullin L., Quollo B., Goldin B.S., Cao Y., Askewazi M., Halling C., Mullin L., Houniel K., Gordon J., Vaudin M., Tarchouk O., Epp A., Liu F., Wollan C., Aitlinger M., Dougherty D., Scott C., Lappas C., Markelz B., Flangan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.;	
RT	RT "Genomic sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58";	
RT	RT Science 294:2317-2323(2001).	
RL	Science 294:2317-2323(2001).	
DR	EMBL: AE009338; AAL4871_1; -	
DR	EMBL: AE008277; AAK89359_1; -	
KW	complete proteome.	
SQ	SEQUENCE 184 AA; 19159 MW; 73D49565A448560B CRC64;	

Query Match 55.8%; Score 43; DB 16; Length 184;
 Best Local Similarity 53.3%; Pred. No. 8.3; 2; Mismatches 5; Indels 0; Gaps 0;
 Matches 8; Conservative

Oy 2 LPMSPRGVASNLXF 16
 Db 54 LPSPKGSVTSGRF 68

RESULT 5

017051 PRELIMINARY; PRT; 631 AA.
 ID 017051 AC 017051; / RIMD 0509952;
 AC 017051; / STRAIN=0157:H7 / PubMed=0509952;
 DT 01-NOV-1996 (TREMBrel. 01, Created)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)

Ascaris lumbricoides (common roundworm).
 Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
 Ascaridae; Ascaris.
 NCBI_TAXID=6252;

[1]

SEQUENCE FROM N.A.

RX MEDLINE=95047480; PubMed=7525414;
 RA Felder H., Herzog A., de Chastagnay Y., Abey P., Tobler H., Müller F.;
 RT "Tas," a proretrovirus-like element from the parasitic nematode Ascaris;
 lumbricoides.", Gene 149:219-225(1994).

[2]

SEQUENCE FROM N.A.

RX MEDLINE=8713498; PubMed=3016762;
 RA Abey P., Spicher A., de Chastagnay Y., Mueller F., Tobler H.;
 RT "Structure and genomic organization of proretrovirus-like elements
 partially eliminated from the somatic genome of Ascaris
 lumbricoides.", Embio J. 5:3353-3360(1986).

[3]

SEQUENCE FROM N.A.

RA Heinz F.H.;
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
 EMBL: Z29712; CA62797.1; -.

DR MEROPS; A16_001; -; -.

DR InterPro; IPR005312; Peptidase_A16.

DR InterPro; IPR001818; Znf_CCIC.

DR Pfam; PP03564; Peptidase_A16; 1.

DR PRINTS; PRO0939; C2HCZNFINGER.

DR SEQUENCE 631 AA; 70684 MW; DBD92609B2705F60 CRC64;

[4]

Query Match 55.8%; Score 43; DB 5; Length 631;
 Best Local Similarity 57.1%; Pred. No. 30; 3; Mismatches 3; Indels 0; Gaps 0;
 Matches 8; Conservative

Oy 1 DPLMSPRGVASNL 14
 Db 432 DPLSPKGSVTSGRF 445

RESULT 6

OBXB29 PRELIMINARY; PRT; 416 AA.
 ID OBXB29; AC OBXB29; DR P97961; / RIMD 182230;
 DR 01-MAR-2002 (TREMBrel. 20, Created)
 DR 01-MAR-2002 (TREMBrel. 20, Last sequence update)
 DR 01-MAR-2002 (TREMBrel. 20, Last annotation update)

Orf, hypothetical protein.
 YID OR_25185 OR EC54659.

Echerichia coli O157:H7.
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 Escherichia; Escherichia1h1; NEBI_TAXID=83334;

[1]

SEQUENCE FROM N.A.

Query Match 53.2%; Score 41; DB 3; Length 1051;
 Best Local Similarity 60.0%; Pred. No. 1.1e-02; PRT;

RC STRAIN=0157:H7 / EDL933 / ATCC 700927;
 RX STRAIN=0157:H7 / PubMed=11206551;
 RA Perma N.T., Plunkett G. III, Burland V., Mau B., Glaser J.D.,
 Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick R.A.,
 Posfai G., Hackett J., Klinsk S., Boutin A., Shao Y., Miller L.,
 Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamitis K.,
 Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.",
 Nature 409:529-533(2001).
 [2]

RP SEQUENCE FROM N.A.

RC STRAIN=0157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11206576;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 Han C.-G., Onitsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 Tada T., Takami H., Honda T., Sasakawa C., Ogawara N., Yasunaga T.,
 Kuwara S., Shiba T., Hattori M., Shinagawa H.;
 RA "Complete genome sequence of enterohemorrhagic Escherichia coli
 O157:H7 and genomic comparison with a laboratory strain K-12.",
 DNA Res. 8:11-22(2001).
 DR EMBL; AE005600; AAG58891.1; -.
 DR EMBL; AP002566; BAB38052.1; -.
 KW Complete proteome.

SEQUENCE 416 AA; 46314 MW; 37D166E852A86669 CRC64;

Query Match 53.2%; Score 41; DB 16; Length 416;
 Best Local Similarity 46.7%; Pred. No. 44; 2; Mismatches 6; Indels 0; Gaps 0;
 Matches 7; Conservative

Oy 2 LPMSPRGVASNLXF 16
 Db 272 LPAPPRGIQVRLLP 286

RESULT 7

P97961 PRELIMINARY; PRT; 1051 AA.
 ID P97961; AC P97961; / RIMD 182230;
 DR 01-MAY-1997 (TREMBrel. 03, Created)
 DR 01-MAY-1997 (TREMBrel. 03, Last sequence update)
 DT 01-MAR-2002 (TREMBrel. 20, Last annotation update)

Peptidole synthetase (Fragment).

OS Cylindrotrichum oligosporum.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariales; Chaetosphaeriaceae; mitosporic Chaetosphaeriaceae;

OC Cylindrotrichum.

OX NCBI_TAXID=72418;

[1]

SEQUENCE FROM N.A.

RA Bernhard F.;
 RT Identification of genes encoding for peptide synthetases from Gram-negative bacteria and filamentous fungi.",
 Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RL EMBL; X96559; CAA5395.1; -.

DR HSSP; PI4687; IAMU
 DR InterPro; IPR000873; AMP-bind.
 DR InterPro; IPR01242; Condensate.
 DR InterPro; IPR03880; Prantne_attach.
 DR Pfam; PF00501; AMP-binding; 2.
 DR Pfam; PF00668; Condensation; 1.
 DR Pfam; PF00550; PP-binding; 1.
 DR PRINTS; PRO154; AMPBINDING.
 DR PROSITE; PS50075; ACP_DOMAIN; 1.
 DR PROSITE; PS00555; AMP_BINDING; 1.
 DR PROSITE; PS00012; PHOSPHOPANTETHENE; UNKNOWN_1.
 FT NON_TER 1051 1051
 FT NON_TER 1051 1051
 SQ SEQUENCE 1051 AA; 116526 MW; 7CB926576B2F0619 CRC64;

OC Ephydriidae; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TRANSPSON=TLGER NON-LTR RETROTRANSPOSON;
 RA Tuschl T., Elbasir S., Lendeckel W.;
 RT "Drosophila melanogaster non-LTR retrotransposon pilger.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AJ27884; CNB9192.1; -
 DR FlyBase: FBgn0041726; pilger\pol.
 DR InterPro: IPR005135; Exo.endo_phos.
 DR InterPro: IPR000477; Rvse.
 DR Pfdm; PR03372; Exo.endo_phos; 1.
 DR Pfdm; PR00078; Rvt; 1.
 KW RNA-directed DNA polymerase.
 SEQUENCE 989 AA; 110315 MW; 5957679C395D79A6 CRC64;
 Matches 6; Conservative 51.9%; Score 40; DB 5; Length 989;
 Best Local Similarity 60.0%; Pred. No. 1.be+02; 4; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PMSPRGVIA 12
 Db 947 PLSPRGLVA 956

RESULT 12

ID 092580 PRELIMINARY; PRT; 1193 AA.
 AC 092580;
 RT 01-FEB-1997 (TREMBrel. 02, Created)
 DT 01-FEB-1997 (TREMBrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE KIAA0268 protein (Fragment).
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BONE MARROW;
 RX MEDLINE=97191544; Pubmed=9039502;
 RA Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayashi Y., Ohara O.,
 RA Tanaka A., Kotani H., Miyama N., Nomura N.;
 RT "Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain.";
 RT DNA Res. 3:321-329(1996);
 EMBL; D87742; BAA13440.1; -.

SEQUENCE 1193 AA; 133704 MW; 70FB2542F9998038 CRC64;

Query Match 51.9%; Score 40; DB 4; Length 1193;
 Best Local Similarity 43.8%; Pred. No. 2.e-02; 7; Mismatches 3; Indels 6; Gaps 0;
 Matches 7; Conservative 50.6%; Score 39; DB 10; Length 112;
 Best Local Similarity 87.5%; Pred. No. 26; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DLPMSPRGVIASNLXF 16
 Db 1113 DLPLHPRGFLPQHAF 1128

RESULT 13

ID 0943R9 PRELIMINARY; PRT; 64 AA.
 AC 0943R9;
 RT 01-DEC-2001 (TREMBrel. 19, Created)
 DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
 DR 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE OSJNBA0083M16.17 protein.

SEQUENCE FROM N.A.
 OC Oryza sativa (Rice).
 OC Oryzaria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoidae; Oryzeae; Oryza.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nippobare(GA3) genomic DNA, chromosome 1, PAC clone: p031D11".
 RT Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AP003211; BAB67893.1; -;
 SQ SEQUENCE 112 AA; 1223 MW; B750B7CA83A448D6 CRC64;

Query Match 50.6%; Score 39; DB 10; Length 112;
 Best Local Similarity 87.5%; Pred. No. 26; Mismatches 1; Indels 0; Gaps 0;
 Matches 7; Conservative 50.6%; Score 39; DB 10; Length 112;
 Best Local Similarity 87.5%; Pred. No. 26; Mismatches 1; Indels 0; Gaps 0;

RESULT 14

ID 0943R8 PRELIMINARY; PRT; 112 AA.
 AC 0943R8;
 RT 01-DEC-2001 (TREMBrel. 19, Created)
 DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE P0031D11.27 protein.
 GN P0031D11.27.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoidae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;

SEQUENCE FROM N.A.

RP STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nippobare(GA3) genomic DNA, chromosome 1, PAC clone: p031D11".
 RT Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AP003211; BAB67893.1; -;
 SQ SEQUENCE 112 AA; 1223 MW; B750B7CA83A448D6 CRC64;

Query Match 50.6%; Score 39; DB 10; Length 112;
 Best Local Similarity 87.5%; Pred. No. 26; Mismatches 1; Indels 0; Gaps 0;
 Matches 7; Conservative 50.6%; Score 39; DB 10; Length 112;
 Best Local Similarity 87.5%; Pred. No. 26; Mismatches 1; Indels 0; Gaps 0;

RESULT 15

ID 091153 PRELIMINARY; PRT; 113 AA.
 AC 091153;
 RT 01-Nov-1996 (TREMBrel. 01, Created)
 DT 01-Nov-1996 (TREMBrel. 01, Last sequence update)
 DT 01-Nov-1996 (TREMBrel. 20, Last annotation update)
 DE Transcription factor (Fragment).

GN MSX-1.
 OS Noctophthalmus viridescens (Eastern newt) (*Triturus viridescens*).
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
 OC Noctophthalmus.
 OX NCBI_TaxID=8316;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MID-BUD OF REGENERATING LIMB;
 RX MEDLINE=95218226; Pubmed=7703517;

RA	Simon H.G., Nelson C., Goff D., Laufer E., Morgan B., Tabin C.; Msi-1 during	GN	MSX-1.
RT	Differential expression of myogenic regulatory genes and Msi-1 during	OS	Notophthalmus viridescens (Eastern newt) (<i>Triturus viridescens</i>).
RT	differentiation and redifferentiation of regenerating amphibian	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
limbs";		OC	Amphibia; Batrachia; Gaudata; Salamandroidea; Salamandridae;
Dev. Dyn. 202:1-12(1995).		OC	Notophthalmus.
-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).		OX	NCBI_TaxID=3316;
DR	EMBL: X82837; CA58044.1; -.	[1]	SEQUENCE FROM N.A.
DR	HSSP; P22808; IPR01356; Homeobox.	RP	SEQUENCE-REGENERATING BLASTEMA;
DR	InterPro; IPR001356; Homeobox.	RC	MEDLINE=95249617; PubMed=7732036;
DR	Pfam; PF00046; homeobox; 1.	RX	Crews L., Gates P., Brown R., Joliot A., Foley C., Brockes J.P.,
PRINTS; PRO024; HOMEBOX.		RA	Gann A.A.; "Expression and activity of the newt Msx-1 gene in relation to limb
DR	PRODOM; PDO00010; Homeobox; 1.	RT	regeneration.,";
DR	SMART; SM00389; HOX; 1.	RT	Regen. Soc. Lond.' B, Biol. Sci. 259:161-171(1995).
DR	PROSITE; PS00027; HOMEBOX_1; 1.	RL	Proc. R. Soc. Lond. B, Biol. Sci. 259:161-171(1995).
DR	PS55071; HOMEBOX_2; 1.	DR	EMBL: X82835; CA57791.1; -.
KW	DNA-binding; Homeobox; Nuclear protein.	DR	HSSP; PI4653; 1B72.
FT	NON_TER 1	DR	InterPro; IPR01356; Homeobox.
SQ	SEQUENCE 113 AA; 12732 MW; 13E442F4858D4982 CRC64;	DR	Pfam; PF00046; homeobox; 1.
Query Match 50.6%; Score 39; DB 13; Length 113;		DR	PRINTS; PRO024; HOMEBOX.
Best Local Similarity 40.0%; Pred. No. 26;		DR	PRODOM; PDO00010; Homeobox; 1.
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;		DR	SMART; SM00389; HOX; 1.
Db 93 MPMSPKGLYAAHVGY 107		DR	PROSITE; PS55071; HOMEBOX_2; 1.
RESULT 16		SQ	SEQUENCE 280 AA; 30966 MW; BBBBD462003CAB7B CRC64;
Q85724 PRELIMINARY; PRT; 150 AA.		Query Match 50.6%; Score 39; DB 13; Length 280;	
ID Q85724		Best Local Similarity 40.0%; Pred. No. 67;	
AC 01-JUN-2002 (TREMBLrel. 21, Created)		Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;	
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)		Db 260 MPMSPKGLYAAHVGY 274	
DE Hypothetical 16.6 kDa protein.		RESULT 18	
GN OSJNBB0091N21.24.		Q981L6 PRELIMINARY; PRT; 442 AA.	
OS oryza sativa (Japonica cultivar-group);		ID Q981L6	
OC Bokarysta; Viridiplantae; Streptophytina; Tracheophyta;		AC 0981L6;	
OC Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae;		DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)	
OC Orychetoidea; Oryzeae; Oryzae.		DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)	
OX NCBI_TaxID=3947; [1]		DE Hypothetical protein mir248.	
RN SEQUENCE FROM N.A.		GN MIR248.	
RP STRAIN=CV_NIPPONBARE;		OS Rhizobium loti (Mesorhizobium loti);	
RC Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,		OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;	
RA Ganssberger K., Brenner M., Burgess S., Hance M., Shvarcbein M.,		OC Phyllobacteriaceae; Mesorhizobium.	
RA Tsitrin T., Riggs F., Hsiao J., Zissmann V., Blunt S., Pai G.,		RN [1]	
RA VanAken S.B., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,		RP SEQUENCE FROM N.A.	
RA Salzberg S.L., White C.M., Fraser C.M., Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.		RC STRAIN=MAF303059;	
RT "Oryza sativa chromosome 10 BAC OSJNBB0091N21 genomic sequence.";		RX MEDLINE=21082930; PubMed=11214968;	
EMBL; AC031122; AAC02695.1; -.		RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,	
Hypothetical protein.		RA Watanabe A., Itohara K., Ishikawa A., Kawashima K., Kimura T.,	
SEQUENCE 150 AA; 16595 MW; 9752C590F7DE4118 CRC64;		RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,	
Query Match 50.6%; Score 39; DB 10; Length 150;		RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpoo S., Sugimoto M.,	
Best Local Similarity 87.5%; Pred. No. 35;		RA Takeuchi C., Yamada M., Tabata S.,	
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		RA "Complete genome structure of the nitrogen-fixing symbiotic bacterium	
QY 2 LPMSPRGV 9		RT Mesorhizobium loti.";	
Db 5 LPLSPRGV 12		RL DNA Res. 7:331-338 (2000).	
RESULT 17		DR EMBL; AP02999; BAB49500.1; -.	
ID 091152 PRELIMINARY; PRT; 280 AA.		DR InterPro; IPR01145; Bac_OmpA.	
AC Q91152;		DR InterPro; IPR01035; MotY.	
DT 01-NOV-1996 (TREMBLrel. 01, created)		DR Pfam; PF00591; OmpA; 1.	
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)		DR PRINTS; PRO01023; NAFGMOTY.	
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)		DR PRODOM; PDO00930; Bac_OmpA; 1.	
DB MSX-1 protein.		SQ KW Hypothetical protein; Complete proteome.	
Query Match 50.6%; Score 39; DB 16; Length 442;		SQ SEQUENCE 442 AA; 47860 MW; 4853A307B1D71850 CRC64;	
Best Local Similarity 60.0%; Pred. No. 1.1e+02;			
Matches 9; Conservative 3; Mismatches 1; Indels 2; Gaps 1;			
Db 1 DLPMSP--RGVIAS 13			

Db 205 | :||| :||||| : 219
RESULT 19
 ID Q9NWBB PRELIMINARY; PRT; 468 AA.
 AC Q9NWBB;
 DT 01-OCT-2000 (TREMBrel. 15, Created)
 DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE Hypothetical 50.2 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo. NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N A.
 TISSUE=EMBRYO;
 Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wagatsu M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa Y., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahashi K., Masuho Y., Ninomiya K., Iwayanagi T., Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 "NEDO human cDNA sequencing project"; EMBL; AK00105; BAA01465.1;
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig-cl.
 DR SMART; SM00409; Ig; 1.
 DR PROSITE; PS00290; Ig_MHC; UNKNOWN_1.
 DR InterPro; IPR003600; Ig-like.
 DR PFAM; PF00047; Ig; 2.
 DR SMART; SM00410; Ig-like; 1.
 DR PROSITE; PS00290; Ig_MHC; UNKNOWN_1.
 SQ 468 AA; 50220 MW; 7C2PC6D5744FB101 CRC64;

Query Match 50.6%; Score 39; DB 4; Length 468;
 Best Local Similarity 37.5%; Pred. No. 1.1e+02;
 Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 Job time : 103 secs

Search completed: January 2, 2003, 12:07:20

QY 1 DLPMSPRGVTASNLXF 16
 :||:||| : : :|
 Db 176 NLPLSPQGTVRTAWEF 191
 :||:||| : : :|

ULT 20
 V59
 Q9BX59 PRELIMINARY; PRT; 468 AA.
 RC 09BX59;
 DT 01-JUN-2001 (TREMBrel. 17, Created)
 DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE PLACE1007632 protein (Hypothetical 50.2 kDa protein).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
 RN [1]
 SEQUENCE FROM N A.
 RP ISSUE=PLACENTA;
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sato H., Sugano S., Shiratori A., Sudo H., Wagatsuna M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa Y., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahashi K., Masuho Y., Ninomiya K., Iwayanagi T.;
 RT "NEDO human cDNA sequencing project";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 SEQUENCE FROM N A.

